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New yeast agglutination genes and yeast contg. them - impart agglutination properties to facilitate removal from fermentation media
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM (SAPB ) SAPPORO BREWERIES.
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  Yeast; agglutination; FLO1L.
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N-PSDB; AAQ71390.
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                      Gaps
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14.4%; Score 938; DB 15; Length 1537;
Best Local Similarity 26.0%; Pred No. 3e-40;
Matches 411; Conservative 244; Mismatches 523; Indels 418;
         Disclosure; Page 43-48; 75pp; English
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977 ggptdetvivirtptseglistttepwtgtftstsaemttvtgtnggptdetvivirtpt 1036 EIVTISST-----KVLPPVVSSNTDLISEPINTREQPTILSTIS-----NSITEDITT 1035 tatvtvsgvtteyttwcpisttettkgtkgttegttettkgttvvtisscesdvcsktas 1316 SQPTGDNGDNTSSTN-.PVPTVATSTLASASEEDNKSGSHESASTSLKPSMGENSGLTTS 1093 1094 TELEATTISPTEAPSPAVSSGTDVTTEPTDTREOPTTLSTT----SKTNSELVATT- 1145 ---QATNENGGKSPSTDLTSSLTTGT-SASTSANSELVTSGSVTGGA 1188 etktvvtsslsrsnhaetqtasatdvighsssvvsvsetgntksltssglstmsggprst 1494 1375 tatvndvvtvyptwrpqtaneesvsskmnsatgetttntlaaetttntvaaet1tntgaa 1434 ------VASASNDQSHSTSV----TNSNSIVSNTPQTTLSQQVTSS 1224 GPPSGTDTVIIREPPNP--TVTTTEYWSQSYATT----TTITAP---PGETDTVLIREPP 686 ggptdetvivirtptseglvttttepwtgtftststemttitgtngvptdetvivirtpt 856 736 YATT----TTVTAPPG-GTD--TVIIREPPNPTV--TTTEYWSQSFATTTTVTAPPGGT- 785 917 ftststemttvtgtngvptdetvivirtptseglistttepwtgtftststevttitgtn 976 786 -----DTVIIYESMSSSKI------STSSNDITSIIPSFSRP------ 816 --HYVNSTTSD-LSTFESSSMNTPTSISSDGMLLSSTTLVTESETT----TELICSDGKE 869 NHTV--TTTEYWSQSYATT----TTVTAPPGE-TD--TVLIREPPNHTV--TTTEYWSQS 735 seglistitepwigtfiststemititgingqpidetviviriptseglistitepwigt 916 TETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSESESKVTFTSNGDNQSGTHDSQSTSTEI 987 CSRLSSSSGIVTNP--DSNESSIVTSTVPTASTMSDSLSSTDGISATSSDNVSKSGVSVT Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer. 1225 SP----STNTFIASTYDGSGSIIQHSTWLYGLITLLSLFI 1260 C899P predicted amino acid sequence. AAM24516 standard; Protein; 5179 AA 12-OCT-2001 (first entry) 40200149716-A2 AAM24516;



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The present invention describes colon tumour associated proteins (I) and the present invention describes colon tumour associated proteins (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by expression or deletions in a patient's genome that affect the patients own production of them. Additionally, (II) may be used to crivity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used or farsociation (PCR) and hybridisation assays to detect and therefore which patients may be in need of restorative therapy. (I) may also be used as an antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies may also be used can an antigen and antagonists may also be used cand in assays to detecting the presence of anti-(I) antibodies and antagonists may also be used cand in an assays to redeeting the presence of TCAPs in samples cand and AMM4494 to AAM4453 represent nucleotide and amino acid sequences and AMM4494 to AAM4453 represent nucleotide and amino acid sequences and antagonists end cand and and antigoriate and an amino acid sequences and antagonists end and amino acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                          Stolk JA;
                                                                                                                                                                                                                                                                                                                                                                                                          Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                  Lodes MJ, Secrist H, Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 446-462; 472pp; English.
                                                            30-DEC-1999; 99US-0476296.
10-ZMN-2000; 2000US-048031.
15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-057521.
29-JUN-2000; 2000US-057521.
28-AUG-2000; 2000US-0649481.
29-DEC-2000; 2000WO-US35596
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King GE,
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1----igdvcg-pgwaaniscratmypdvpigqlgqtvvcdvsvglicknedqkpggv 1860 273 RPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTR 332 59 TSANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDAL 118 119 KSSIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTV 178 DP---SAYLYASRVMPSLNKVT-----TLFVAPQCE-NGY-TSGTMGFSSSNGDVA 224 Ouery Match 11.1%; Score 721.5; DB 22; Length 5179; Best Local Similarity 25.3%; Pred No. 2.1e-28; Matches 335; Conservative 158; Mismatches 554; Indels 279; Gaps 225 IDCSNIHIGITKGLNDWNYPVSSESFSY-----TKTC-TSNGIQIKYQN-VPAGY 179 1808 g g ò ò ò ð

2831 ptptgt 2836

1128 -----PTTLSTTSKTNSELVATTQAT----NENGGKSPSTDLTSSLTTGTSASTSANSELV 1179 2711 tvtptptptgtgtgtttttttttvtptptptgtgtptttpittttvtptptgtgtgt 2770 1180 TSGSVTGGAVA----SASNDQSHSTSVTNSNSIVSNTPQTTLSQQVTSSSPSTNTFIAST 1235 2133 ttttvtptptptgtqtptttpittttvtptptptgtqt-----ptttpittt----- 2180 2181 -ttvtptptptgtgt-----ptttpittt-----ttvtptptptgtgtgtttpittt 2226 981 QSTSTELEIVTTSSTKVLP------PVVSSNT-DLTSEPINTREQPTTLSTTSNS 1028 2322 tptptptgtgtp-tttp1ttttvtptptptgt----qtptttp1ttt----ttvtptpt 2372 1029 ITEDITTSQPTGDNGDNTSSTNPVPTVATST-LASASEEDNKSGSHESASTSLKPSMGEN 1087 tptptptgtgtgttttpitttttvtptptptgtgtptttpittttvtptptptgtgtgtt 1967 2025 tptptgtgtp-tttp1ttttvtptptptgt---qtptttp1ttt-----ttvtptp 2072 2273 tivipipipigi---gipitipiiti-----tivipipipigiqipitititis 2321 433 LPNPTVSTTEYWSQSFATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFATTTTVTA 492 493 PPGGTD-----SVIIREPPNPTVTTTEYWSQSFATTTTVTAP---PGGTD-----S 535 536 VIIREPPNPTVTTTEYWSQSYATTTTVTAP---PGGTDSVIIREPPNHTVTTTEYWSQSY 592 593 ATTITVTAPPGGIDIVIIREPPNHIVTTIEYWSQSFATITIVTGPPSGTD-----T 643 644 VIIREPPNPTVTTTEYWSQSYATTTTTTAPPGETDTVLIREPPNHTVTTTEYWSQSYATT 703 TTVTAPPGETDTVLIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTD------TVII 754 755 REPPNPTVTTTEYWSQSFATTTTVTAPPGGTDTVIIYESMSSSKISTSSNDITSIIPSFS 814 815 RPHYVNSTTSDLSTFESSSMNTPTSISSDGMLLSSTTLVTESETTTELICSDGKECSRLS 874 875 SSSGIVTNPDSNESSIVTSTVPTASTMSDSLSSTDGISATS--SDNVSKSGVSVTTETSV 932 933 TTIQT-----TPNPLSSSVTSLTQLSSIPSVSESESKVT---FTSNGDNQSGTHDS 980 TVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTTITTSYVGVTTSYLTKTAPIG-ETATV 391 1088 SGLTTSTEIEATTTSPTEAPSPA-----VSSGTDVTTEPTDTREQ-----392 IVDVPYHTTTTVTSEWTGT------ITTTT-1236 YDGSGS 1241 1908 g QQ QQ ò qq δ QΩ ò qq δy рp δ QQ ò q ò a ò Pp ò Q δ 셤 à QQ ò ò g ò ρp δ ó ò

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212 GTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQNVPAG 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511); expressed DNA sequences (ABL5173-ABR3072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDAL---KSSIKAFGTV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 TLPIAFNVGGTGSSTD-------LEDSKCFTAGTNTVTFNDGDKDISID-- 170
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                                                                                                                              developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.5%; Score 685; DB 22; Length 2586;
Best Local Similarity 24.7%; Pred. No. 6.88-27;
Matches 405; Conservative 183; Mismatches 557; Indels 494,
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 27426; 21pp + Sequence Listing; English.
                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 27426
                                                                                                                                                                                                                                                                                                                       Myers EW;
                                  ABB66878 standard; Protein; 2586 AA
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                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                (first entry)
                                                                                                                                                                Drosophila melanogaster.
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249

993 dnsst----qsssstttttssdeggatsssapvvdlsggsssngdgnstgssttttittt 1048 .049 tssdgdqsttssdpvvevsqgtnggnsstqsssstttttssdegqttssfgscrrshsri 1108 1109 lfqcprqrqqlqrrhlpmvanppphltpvvevsqgtngdnsstqsssstttttssdeggt 1168 TTLSTTSNSITEDITTSQPT----GDNGDNTSSTNPVPTVATSTLASASEEDNKSG--- 1071 616 553 585 629 932 272 YRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAG-----SNGIV 326 ------evaggsssngdgnstgsst-ttttttttssdgggsttssdpvv 409 327 IVA-----TTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTTTTSYVG----- 373 374 -VTTSYLTKTAPIGETATV----IVDVPYHTTTTVTSEWTGTITTTTRTN---PTDSID 425 525 pvvevaggsssngdgnstg--satttttttttssdgggsttssdpvveasggtnggnsst 582 : : | ||| |: ||| || |- ||| |- ||| |- ||| |- ||| |- ||| |- ||| |- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- ||- | 757 | : | | | : | | | pttsssdpvvevaggsssngdgnstqssttttttttttssdggesttssdpvvevsggtng 817 818 dnsstq--sssstttttssdegqttsssdpvsevaqgssstgdgnstqsstttttttd1 875 W---SQSYATTTTTTAPPGETDT-----VLIREPPNHTVTTTEYWSQSYATTTTVTAPPG 711 712 ETDT-----VLIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDT-----VIIREPPNP 760 761 TVTTTEYWSQSFATTTTVTAPPGGTDT-----VIIYESMSSSK---ISTSSNDITSIIPS 812 813 FSRPHYVNSTTSD-----LSTFESSSMNTPTSISSDGMLLSSTTLVTESETTT 860 IQTTP-----KVTFTSN 970 309 ttttttssdgggsttlsdpvvevsggtnggnsstgsssstttttssdeg-gttsssdpvg 367 410 evsqgtnggnsstgsssatttt----ssdegqttsssdpvsevaggsssigdgnstgs 464 465 stttttttttssdgggsttssdpvvevsggtnggnsstgsssstttttssdeggttsssd 524 426 TV--VVQVPLPNPTVSTTEYWSQSFATTTTVTAPPGG-----TDTVI------IR 467 876 frcprqrttttttssadggesttlsdpvvevsggtnggnsstg---ssssttttssadeg TDSVIIREPPNPTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVTTTEYWS---698 dgnstqssttttttttttssdgggsttlsdpvvegsggtnggnsstgsssstttttssdeg -----EYWSOSYATTTTVTAPPGGTDT-----VIIREPPNH TVTTTEYWSQSFATTTT---------VTGPPSGTDTVIREPPNPTVTTEY 891 VTSTVPTASTMSDSLSST--DG-ISATSSDNV-----SKSGVSVTTETSVTT GDNQSGTHDSQSTSTEIEIVTTSS----TKVLPPVV----SSNTDLTSEPTNTREQP 554 -----QSYATTTVTAPPGGTDSVIIREP--------PNHTVTTT----1020

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Sequence
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                                                                                                                                        1094 TEIEATTTSPTEAPSPAVSSGTDVTTEPTDTREQPTTLSTTSKTNSE-----LVA 1143
                                                                                                  sd-eggtts-ssapvvdisggsssngdgnst-gssttttttttttssdggesttlsdpvve 1516
                                                                                                                          1144 TTQATNENGGKSPSTDLTSSLTTGTSA----STSANSELV------TSGSVT 1185
                                                                                                                                                                      1186 GGAVASASNDQSHST------SVTNSNSIVSNTPQTTLSQQVTSSSPST 1228
                                                                                                                                                                                            1574 tttttttssdggesttssdpvvevsggtngdnsstgsssstttttssdeggttsssdpvv 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr GJ;
                                                       1400 disqgsssnvldndnnynddifrwwanpppyltplwksvkegmaitaplslrrppgggts
                                  --SHESAS-----TSLKPSMGENSGLT-----TS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus cellular proliferation protein #1290.
                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Seq ID No 12713; 511pp; English.
                                                                                                                                                                                                                                                                                                AAU37120 standard; Protein; 2344 AA
                                                                                                                                                                                                                   1229 NTFIASTYDGSGSIIQHST 1247
                                                                                                                                                                                                                                          1634 evaggsssngdgnstgsst 1652
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2000US-253625P.
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2001US-269308P
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haselbeck R, Ohlsen KL,
Yamamoto RT, Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus
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N-PSDB; AAS54979.
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for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antibodies capable of sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of cryanisms. The present sequence represents an essential prokaryotic callular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formed in the published poct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VDVPYHTTTTVTSEWTGTITTT----TRINPIDSIDTVVQVPLPNP 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 ----kvmtvkyaggtwtrnisdwiaksgttnfslsmtastgg-atnlggvqfg--- 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 YTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKSSIK------AFGTV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 -vlgetglngaavgigglsnaf--gfkldtyhn-tstpnssakakadpsnvaggafgaf 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 TLPIAFNVGGTGSSTDLED--SKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAYLYA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 640.5; DB 22; Length 2344;
Pred. No. 1.2e-24;
9; Mismatches 542; Indels 323; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::| | :|: | | :| | 396 vttdsygvastytssstadnaaklnvqptnn-tfqd-----fdinyngdt------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 SRVMPSLNKVTTLFVAPQ-----CENGYTSGTMGFSSSNGDVAIDCSNIHIGITK
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Best Local Similarity 22.2%; Promatches 323; Conservative 269;
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1234 stslsdansesgststslsnstsgsasiststsgsaststvksesvstslststslsd 1293
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                                                                                                                                                                                                                                                                                                                                               1012 PINTRE--OPTILSTISNSITEDIITISOPT--GDNGDNISSTNPVPIVATSTLASASEED 1067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTSASTSANSELVTSGSVTGGAVASASNDQSHSTSVTNSNSIVSNTPQTTLSQQVTSSS 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1593 tsladsqsts---rstsasgsastststsdsrstsaststsmrt---stldsgsmsls 1644
                                     APPGETDTVL----IREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVIIREPPNPTV 762
                                                                                       TTTEYWSQSFATTTTVTAPPGGTDTVIIYESMSSSKISTSSNDITSIIPSFSRPHYVNST 822
                                                                                                                                        TSDLSTFESSSMNTPTSIS-----SDGMLLSSTTLVTE-----SETTTELICSDGKE
                                                                                                                                                                                           908 TDGISATSSDNVSKS----GVSVTTETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
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ABB69806 standard; Protein; 1795 AA.
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11-JUL-2000; 2000US-0614150.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invention useful in developmental belotogy and in elucidating cell signalling and interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmacoutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA (ABB57737-ABB72072).

The sequence for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO at ftp.WiPpo.int/pub/published_pct_sequences.
                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more spense from brosophila and for elucidating cell signalling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 gtifspverkclpgdqcpstelsdsgsylpgncelkfpecaeegtf----rsptdcaly 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 -ytcrlqesgtylqtrfkcp---gsnsfdlerklcrprsevdcfdfvpg----- 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 LYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNY 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 KTAPIGETATV------IVDVPYHTTTTVTSEWTGTITTTTR---TNPTDSID 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stttp----stttpsttttpsttttykv---sthrprttsgktttastttkktttspk 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    603 GGTDTVIIREPPNHTVTTTE---YWSQSFATTTTVTGPPSGTDTVIIREPPNPTVTTTEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 322;
                                                                                                                                                          Disclosure; SEQ ID NO 36210; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1795;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.3%; Score 601; DB 22; Best Local Similarity 24.7%; Pred. No. 9.4e-23; Matches 323; Conservative 162; Mismatches 499;
               Myers EW;
               PWD,
               Ľ
             Adams M,
                                           WPI; 2001-656860/75.
N-PSDB; ABL13909.
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           Venter JC,
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703 TTTVTAPPGETDTVLIRE----- 729
                                                                                                                        Example 1; Page 131-139; 142pp; English.
               Sternberg PW, Barr MM;
                                       WPI; 2000-452537/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 290; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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1192 sttppsrehaptqrpsssqpsssqrsrgvtiaqmarhnlatskpflahslrlsiqqlastq 1251
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                                                                                                                                                                                                                                                                                         1014 ttvivstqnpttttsktstvtittpnpspstgrpttttrqptsitasttsigttripttt 1073
                                                                                                                                                                                                                                                                                                                  QP-----TGDNGDNTSSTNPVPTVATSTLASASEEDNKSGSHE 1074
                                                                                                                                                                                                                                                                                                                                         1074 npqnstsstdlttvtrppcpdpdstsdkntntactgelggv--nllelgspgkgegftht 1131
                                                                                                                                                                                                                                                                                                                                                                1075 SASTSLKPSMGENSG------LTTSTEIEATTTSPTEAPSPAVSSGTD-----V 1117
                                                                                                                                                                                                                                                                                                                                                                                        1132 rthtaltgsrntlggqevpdymddapssaeaesggattakaptmstlaaahllgklfhii 1191
                                        826 LSTFESSSMNTPTSISSDGMLLSSTTLVTESETTTELICSDGKECSRLSSSSGIVTNPDS 885
                                                                                                                                                                  886 NESSI----VTSTVPTASTMSDSLSSTDGISATSSDNVSKSGVSVTTE----TSVTTI-- 935
                                                                                                                                                                                     693 stesspkptsstgkptttpkpstrttptttkvttttqittttplrsstettstgppttt- 751
                                                                       TTTV-----TAPPGGTDTVIIYESMSSSKISTSSND--ITSIIPSFSRPHYVNSTTSD 825
                                                                                           798 ttkvalttgkettptgststtiftrktttnnpeptstekpitsttp---kp---stttpk 851
                                                                                                                                           852 tstvasst--ekttissp---kpttekstenpttnsv-----ktsaltsstgratstts 900
                                                                                                                                                                                                                  ---OTTPNPL-----SSSVTSLTQLSSIPSVSESESKVTFTSNGDNQSGTHDSQST--- 983
                        715 TVLIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVIIREPPNPTVTTTEYWSQSFAT 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).
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isolated nucleic acid molecules from Caenorhabditis elegans useful for producing transgenic nematodes with altered mating behavior for identifying genes or regulatory factors involved in polycystic kidney disease.
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1140 sgsgsggsstgsgaggsgttasggsggssgtgsdgvnsgkttalngdgtgsgtattpgs 1199
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                                                                                                                                                                                                                                                                                                                     SSTK------VLPPVVSS-----NTDLTSEPTNTREOPTTLSTTSNSITEDITTSOPTG 1040
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                                                                                                                                                                                                                                                                        946 VISLTQLSSIPSVSESESKVTFTSNGDNQSGTHDSQSTST------EIBIVTT 992
                                                                                                                                                 755 qfdfildsglswnetrhnedsinivplptnaltpter--sqtfecrnvstepfliikest 812
                                                                                                                                                                                                   813 clnysntvlnatyssnipiqpietflvgigtyefrinmtdlttmqvvshiftlnvvadst 872
                                                                                                                                                                                                                         887 ESSIVTSTVPT-ASTMSDSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLSSS 945
                                                                                                                                                                                                                                           836 TPTSISSDGMLLSST------TLVTESETTTELICSDGKECSRLSS------ 875
                                                                                                                                                                            988 NSG----- 886
                                                    645 ytyanvyiqeysstliesesstaavasatsst----pstpsstlststvtepsstrssds 700
                                                                               776 TTVTAPPGGTDTVIIYESMSSSKISTSSNDITSIIPSFSRPHYVNSTTSDLSTFESSSMN 835
                                                                                              730 ----EYWSQSYATIT-----TVTAPPGGIDTVIIREPPNP-----TVTTEYWSQSFAIT
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                                                                                                                                                                                  ------SSGIVTNP-----
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The present sequence is that of the polypeptide encoded by the caenorhabdits elegans LOV-1 gene (see AAA50043), an orthologue of the human polycystin. (RKD1) gene that is defective in human the control of the control
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                                                                                                                   Isolated nucleic acid molecules from Caenorhabditis elegans useful for producing transgenic nematodes with altered mating behavior for identifying genes or regulatory factors involved in polycystic kidney
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                                                                                                                                                                                                                                                              Claim 5; Page 114-123; 142pp; English.
            Barr MM;
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                                                                WPI; 2000-452537/39.
N-PSDB; AAA50043.
                   Sternberg PW,
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SSTK-----VLPPVVSS----NTDLTSEPTNTREQPTTLSTTSNSITEDITTSQPTG 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1087 pttt--tetppttvsssddaggktggtgatggtggtgsggsattlst----gdavrstt 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1147 ATNENGGKSPSTDLTSSLTT----GTSASTSANSELVTSGSVT-------1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1041 DNGDNTSST--NPVPTVATSTLASASEEDNKSGSHESASTSLKPSMGEN-SGLTTSTEIE 1097
                                                                                                                                                                                                                                                                                                             Mucin; MUCil; MUCil; human; chromosome 7q22; epithelial inflammation; Crohn's disease; ulcerative colltis; asthma; chronic bronchitis; colorectal cancer; cystic fibrosis; inflammatory bowel disease; breast cancer.
                                              645 ytyanvyiqeyssttlesesstaavasstsst----pstpsstlststvtepsstrssds 700
                                                                                                                                                  988 NSG------SSGIVINP-----BSN 886
                                                                                                                                                                                                                                       887 ESSIVTSTVPT-ASTMSDSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLSSS 945
                                                                                                                                                                                                                                                        946 VTSLTQLSSIPSVSESESKVTFTSNGDNQSGTHDSQSTST------EIEIVTT 992
                           730 ----EYWSQSYATTT-----TVTAPPGGTDTVIIREPPNP-----TVTTTEYWSQSFATT 775
                                                                                              813 clnysntvlnatyssnipigpietflvgigtyefrinmtdlttmgvvshiftlnvvadst 872
585 siectsptssnyvsttkdgacftksvsmprlggtypastfvgpgnytfratmttddkkvy 644
                                                                          776 TTVTAPPGGTDTVIIYESMSSSKISTSSNDITSIIPSFSRPHYVNSTTSDLSTFESSSMN
                                                                                                                               836 TPTSISSDGMLLSST-----TLVTESETTTELICSDGKECSRLSS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1186 ----GGAVASASNDQSHSTSVTNSNSIVSNTPQTTLSQQV----TSSSPSTNT 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY59288 standard; Protein; 957 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human MUC11 polypeptide.
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Modified-site
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The invention provides mucin genes (MUCI1 and MUCI2) located on human chromosome 7422. The mucin genes or its portion is used in detecting polymorphism, mutation, deletion, truncation and expansion in the gene or its gene transcript. Pharmaceutical compositions and gene therapy constructs comprising the mucin genes are used for treating disease occiditions associated with aberrant Mucin expression, altered properties of mucus or epithelial inflammatory processes involving Mucins ilke colorectal cancer, cystic fibrosis, inflammatory browel disease and cancer. The mucin genes and the polypeptides are used for determining these diseases or theat predsposition. The MUCI1 and MUCI2 polypeptides are used for preparing antagonist and antibodies. The present sequence represents the human MUCI1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
                                                                                                                                                                                                          Novel MUC nucleic acid corresponding to mucin gene, useful for treating associated disease conditions e.g. colorectal, breast cancer, cystic fibrosis and inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 tthtissap-sttsalveeptsyhsspgstatthfpdssttsgrseestashsngdatgt 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 stettllpdnttasglleastpvhsstgsphttl----spagsttrggesttfgswpn 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFATTTTVTAPPGGTDTVIIREPPNH --- TVTTTEYWSQSFAT ---- TTTVTAPPGGT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 DSVIIREPPNPTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSYA 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 att----psparstt---sglveesttyhsspgstqtmhfpesdttsgrgeesttshss 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         598 VTAPPGGTDTVIIREPPNHTVTTTEYWSQSFATT----TTVTGPPSGTDTVIIREPPNPT 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         654 VITTEYWSQSYAT---TITIITAPPGETDTVLIREPPNHTVTTTEYWSQSYAITITVTAPP 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 215; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 ttafpgsttmpgvsqestas--hsspgstdttlspgstta----sslgpesttfhsgpg
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                                                   (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
(ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
                                                                                                                Antalis TM, Mcguckin MA, Gotley
                                                                                                                                                                                                                                                                                       Claim 10; Page 83-88; 103pp; English
                98AU-0004708
                                                                                                                                                    WPI; 2000-182416/16.
N-PSDB; AAZ58824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         957 AA:
                                                                                                              Williams SJ,
                16-JUL-1998;
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1001 VVS--SNTDLTSEPTNTR------EQPTTL-----STTSNSITEDITTS--- 1036
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                                                                                                             941 PLSSSVTSLTQLSSIPSVSESESKVTFTSNGDNQSGTHDSQSTSTEIEIVTTSSTKVLPP 1000
                                                                                                                                                                                                                                                                                                                                                                                        1165 --TTGTSASTSANSELVTSGSVTGGAVASASNDQSHSTSVTNSNSIVSNTPQTTLSQQVT 1222
                   PDSNESSIVTSTVPTAS--TMSDSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPN 940
                                                                             sghsekstifhsspdasgttpssahsttsgrgesttsrispgsteittlpgst---ttpg 597
                                                                                                                                       598 -lseasttfyssprsptttlspasmtslgvge-esttsrsqpgsthstvspastt---tp 652
                                                                                                                                                                                        770
                                                                                                                                                                                                                                                                                                771 tpsrlspsstetttlpgspttpslseksttfytsprspdatlspatttssgvseesstsh 830
                                                                                                                                                                                                                                                                                                                                                                                                          823 TSDLSTFESSSMNTPTSISSDGMLLSSTTLVTESETTTELICSDGKECSRLSSSSGIVTN 882
                                                                                                                                                                                                                                         -----SPTEAPSPAVSSGTDVTTEPTDTR
                                                                                                                                                                                                                                                                                                                                 EQPTTLSTTS------KTNSELVATTQATNENGGKSPSTDLTSSL-----
                                                                                                                                                                                                                                                                                                                                                       Stolk JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lodes MJ, Secrist H, Benson DR, Meagher MJ, ,, Wang T, Jiang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C900P predicted amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM24513 standard; Protein; 957 AA.
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10-JAN-2000; 20000US-0480312.
15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0575231.
29-JUN-2000; 2000US-059481.
28-AUG-2000; 2000US-0649811.
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The present invention describes colon tumour associated proteins (I) and the present invention describes colon tumour associated proteins (I) and (II) can be used in the foreign describe accine production. (I) and (II) can be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TGAP) expression, such as colonic cencer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by captients on production of them. Additionally, (II) may be used to trutaring the cell colonic cencer. For example, (I) and (II) may be activity of TGAP by expressing inactive proteins or to supplement the activity of TGAP by expressing inactive proteins or to supplement the cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and therefore which patients may be in need of restorative thereby. (I) may the used as antigens in the production of antibodies and antagonists may also be used to down require.

TGAP expression and activity. The anti-(I) antibodies and activity. The anti-(I) antibodies and antagonists may also be used to down require a diagnostic agents for detecting the presence of TGAP expression and activity. The anti-(I) antibodies also be used as an antigen in the presence of TGAP in samples of e.g. by enzyme linked immunosorbant assay (EISA). AA128460 to AAA129512 and AMA4494 to AAA44523 represent nuclectide and amino acid sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Quest Local Similarity 25.98, Pred No. 3.5e-20;
Matches 266; Conservative 139, Mismatches 406; Indels 215; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 HTTTTVTSEWT---GTITTTTTTTRTNPTDSIDTVVVQVPLPNPTVSTT------EYWSQ 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498 DSVIIREPPNPTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSYA
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                 Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer -
                                                                                Claim 2; Page 437-440; 472pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 QVPLPNPTVS-TTEYWSQSFATT----TTVTAPPG-GTD--TVIIREPPNH--TVTTTEY 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 WSQSFATT----TTVTAPPG--GTDSVIIREPPNPTVTTTEYWSQSFATTTVTA---- 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    585 TEYWSQSYATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFATTTTVTGPPSGTDTV 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              svi--sssvtsslvts----tsts 277
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                                                               AAW06725 is the FLOI protein derived from a partial gene sequence from Saccharonyces cerevisiae. The gene was named Lg-FLOI. The FLOI protein is believed to be involved in yeast flocculation (aggregation). The DNA and protein are used in a method for determining whether or not a sample yeast has flocculating activity, i.e. to distinguish if a yeast is a flocculating or floating yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tngqptdet-vivvktpttantivtttkpwtgtftststemttvtgtngqptde-tvivi
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8.2%; Score 534; DB 17; Length 849;
Best Local Similarity 26.0%; Pred No. 1.1e-19;
Matches 244; Conservative 152; Mismatches 386; Indels 156;
                     Claim 1; Page 6-10; 16pp; Japanese
                                                                                                                                                                                                                                                   849 AA;
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                                                                                                                                                                                                                                                                                                                        1001 VVS--SNTDLTSEPTNTR------EQPTTL-----STTSNSITEDITTS--- 1036
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                                                                  492 stafqthpasthttpst-----pstatapveesttyhrspsstptthfpass---tt 540
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                  823 TSDLSTFESSSMNTPTSISSDGMLLSSTTLVTESETTTELICSDGKECSRLSSSSGIVTN 882
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/note= "partial sequence only, no start codon"
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N-PSDB; AAT45666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The flocculation protein is used in a method to immobilise enzymes to a microbial cell wall. The coding sequence (FLO 1) is used in the production of a recombinant polynuclectide which comprises a structural gene encoding a protein with catalytic activity and at least part of a gene encoding at least the C terminus of a protein capable of anchoring fragment or protein is selected from alpha aggluthin, anchoring fragment or protein is selected from alpha aggluthin, canchoring fragment or protein is selected from alpha aggluthin, preferably also comprises a sequence encoding a signal peptide to preferably also comprises a sequence encoding a signal peptide to preferably derived from glycosyl-phosphatidy1-inosito, anchoring protein, alpha factor, alpha-aggluthin, invertase or inulinase, alpha-amplase of Bactilus or proteinsses of lactic acid bactilus or proteinses or fundinase, alpha-amplase of Bactilus or proteinsses of lactic acid bacteria.

The host microorganism can be used for performing enzymatic
1165 TTGTSASTSANSELVTSGSVTGGAVASASNDQSHSTSVTNSNSIVSNTPQTTLSQQVTSS 1224
                    Immobilisation; enzyme; cell wall; alpha agglutinin; AGA 1; FLO 1; Major cell wall protein; glycosyl-phosphatidyl-inositol; anchoring protein; alpha factor; alpha-agglutinin; invertase; inulinase; alpha-amylase; Saccharomyces cerevisiae; floculation protein; enzymatic process; fermentation; blodegradation; callysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immobilisation of enzymes to microbial cell wall - by prodn. of
fusion protein of enzyme linked to anchoring protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 894;
                                                                                                                                                                                                                                                            Flocculation protein of Saccharomyces cerevisiae.
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7.9%; Score 516; DB 15;
Best Local Similarity 26.3%; Pred. No. 9.8e-19;
Matches 251; Conservative 126; Mismatches 310.
                                                           1225 SPSTNTFIASTYDGSGSIIQHSTWLYGLITL--LSLFI 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Verrips CT;
                                                                            || : || | : || | 814 --stasleistyvgian-----glltnngisvfi 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 10; Page 59-64; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toschka H,
                                                                                                                                                                   AAR47578 standard; Protein; 894 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92EP-0202080.
                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klis FM, Schreuder MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       894 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ54029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1992;
14-DEC-1992;
                                                                                                                                                                                                                                19-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                 AAR47578;
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43;

Indels 266;

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1048 STNPVPTVATSTLASASEED--NKSGSHESASTSLKPSMGENSGLTT----STEIEATT 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1101 TSPT-----EAPSPA-VSSGTD----VTTEPTDTREQPTTLSTTSKTNSELVAT 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1145 TQATNENGGKSPSTDLTSSLTTGTSASTSANSELVTSGSVTGG----AVASASNDQSHS 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    577 lvtsattsgetasslppatttkt-----seqttlvtv------tsces 613
                                                                                                                                                                                                                                                                                                                                                                              205 egtvymyagyyypmkvvysnavswgtlpisvtlpdgttvsddfegyvysfdddisgsnct 264
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                                                                                                                                                                                                                                                                             158 tyddsailsyggatafnccaqqqppitstnf----tidgikpwggs-----lppn1 204
                                                                                                                                                                                                                                                                                                                                   581 TVTTTEYWSQSY-----DTVI 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 tepwtgtftststevtt1tgtngqptdetv1v1rtptsegl1stttepwtgtftststem 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             704 TIVTAPPGEIDIVLIREPPNHIVITIEXWSQSYATITIVIAPPGGIDIVIIREPPNP--T 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 csnsqgiaywstdlfgfytt------ptnvtlemtgyflppqtgsytfkfa
                                                                                                                                                                                                                       522 TT-TTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSYATTTTVTAPPGGTDSVIIREPPNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                  610 IREPPNH----TVTTTEYWSQSFATT----TTVTGP---PSGTDTVIIREPPNPTV--TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 657 TEYWSOSYATT----TTITAPPGE-TD--TVLIREPPNHTV--TTTEYWSQSYATT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        762 VITTEYWSQSFATITIVTAPPGGT-----DIVIIYE----SMSSSKISISSNDITSIIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           812 SFSR----PHYVNSTTSDLSTFESSSMNTPTSISSDGMLLSSTTLVTESETTTELICSDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529 skssviptssstsgssesetss-----agsvssssfissessksptyssslp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  928 TETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSESESKVTFTSNGDNQSGTHDSQSTSTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1200 TSV-----TNSNSIVSNTPQTTLSQQVTSSSP-----STNTFIASTYDGSGS 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437 TVSTTEYWSQSFATTTTVTAPPGGTDTVIIREPPNHTVTTT----
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AAR58754
ID AAR5
XX
AC AAR5
XX
DT 27-M
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762 VTTTEYWSQSFATTTTVTAPPGGT-----DTVIIYE----SMSSSKISTSSNDITSIIP 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB40945 standard; Protein; 1532 AA
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02-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Valuable compounds are isolated from complex mixtures by use of immobilized ligands composed of an anchoring protein and a binding protein. A sultable anchoring protein is yeast FLO1 (associated with flocculation), and a gene encoding a chimeric scPv-FLO1 protein that will anchor in the cell wall of a lower eukaryote, and which binds HCG with high specificity, was produced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.9%; Score 516; DB 15; Length 894;
llarity 26.3%; Paged, No. 9.8e-19;
Conservative 136; Mismatches 310; Indels 266; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              437 IVSTIEYWSQSFATTTTVTAPPGGTDTVIIREPPNHTVTT-----------------477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 csnsqglaywstdlfgfytt------ptnvtlemtgyflppqtgsytfkfa 157
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                                                                                                                                                                                                                                                                                                                                                            Immobilised binding proteins for specific cpds - obtd. by expressing chimeric proteins comprising the binding protein and a cell wall-anchoring protein in host cells
                                      Binding protein; immobilization; chimeric protein;
anchoring protein; Saccharonycas cerevisiae; flocculation;
FLOI gene; serv; single chain antibody; monoclonal antibody;
MAD; human chorionic gonadotropin; HGG:
                                                                                                                                                                                                                                                                                             Toschka HY, Verrips CT;
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 36-39; 78pp; English.
                                                                                                                                                                                                                                                                                             Klis FM,
                                                                                                                                                                                             94WO-EP00427.
                                                                                                                                                                                                                     93EP-0200350.
                                                                                                                                                                                                                                                                                             De Geus P, Frenken LGJ,
                                                                                                           Saccharomyces cerevisiae
                                                                                                                                                                                                                                                  (UNIL ) UNILEVER NV.
                                                                                                                                                                                                                                                                                                                      WPI; 1994-279751/34.
N-PSDB; AAQ67360.
           S. cerevisiae FLO1
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                                                                                                                                                                                           10-FEB-1994;
                                                                                                                                                                                                                     10-FEB-1993;
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Best Local Simi
Matches 251;
                                                                                                                                    WO9418330-A.
                                                                                                                                                                18-AUG-1994.
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; antiporotatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antivibatical; antibacterial; antifungal; antirhemmatic; antithyrod; antidiancerial; antifungal; antirhemmatic; antithyrod; neurodegenerative discorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; blacky; aplastic annemia; nocturnal haemoglobinuria; burn; wound; thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          988 EIVTTSSTKVLPPVVSSNTDLTSEPTNTREQPTTLSTTSNSITEDITTSQPTGDNGDNTS 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .048 STNPVPTVATSTLASASEED -- NKSGSHESASTSLKPSMGENSGLTT ----STEIEATT 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             663 ettkqttvvt---isscesdvcsktaspalvststatingvtteyttwcpisttesrqqt 719
928 TETSVITIQITPNPLSSSVISLIQLSSIPSVSESESKVIFISNGDNQSGTHDSQSTSTEI 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           577 lvtsattsgetasslppatttkt...-segttlvtv...--tsces 613
                                                                                                                                                        | || ;;;;;;;;|
780 t--tntlaaetttntvaaetitntga---aetktvvtsslsrsnhaetqtasatdvighs
                                                                                                     812 SFSR----PHYVNSTTSDLSTFESSSMNTPTSISSDGMLLSSTTLVTESETTTELICSDG
                                                                                                                                                                                                                                                         868 KECSRLSSSSGIVTNPDSNESSIVTSTVPTASTMSDSLSSTDGISATSSDNVSKSGVSVT
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1237 DGSGSIIQHST 1247
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                                                                                                                                                                                                                                                                                AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatorropic; vulnerary; antiparkinsonian; nociropic; neuroprotective: osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; antidiamatory; antibacterial; antivital; antifungal; antithematic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or prevancing or treating can be used to express ORFX proteins in gene therapy to each or and entering and nucleic acids can be used to express ORFX proteins in gene therapy or coctors. The proteins and nucleic acids may be used to treat cancers, or occors. The proteins and nucleic acids may be used to treat cancers, or occors. The proteins and nucleic acids may be used to treat cancers, or occors. The proteins and nucleic acids and ideasace, octaoparthritis, the presence of or predisposition to disease, occorationed immunodeficiency (SCID), AIDS, viral, altypertension, hypothyroidism, cholesterol ester storage, systemic lupus cythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, cocturnal haemoglobinuria, antinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sqqi----ttapstnh---stihststspqespa---vsqrghtqapqttqesqttrsv 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 338; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVNDALKSSIKAFGTVT-----LPIAFNVGGTGSSTDLEDSKCFTAGTNTV---- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 svettrvsgintlntltpvttstvlsspsgfnpsgtvs----getfpsgettisspss 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---KVTTLFVAPQCENGYTSGTMGFSSS-NGDVAIDCSNIHIGIT------KGLNDWNY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P--VSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTC--- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    telpststgaatrlvtgnp----stgaagtiprvpskvsaigepgepttysshsttlpk 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AGSRLQSKPFTLRWTGYKNSDAGSNGIVIVAT-TRTVTDSTTAVTTLPFNPSVDKTK 354
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                                                                                                                                                                               Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 lppkistafhtggsegaettgrpherssfspgvsgeiftlhetttwpssfsskghttwsg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 7.8%; Score 507; DB 21; Seet Local Similarity 23.3%; Pred. No. 5.6e-18; Matches 324; Conservative 200; Mismatches 529,
                                                                                                                                                                                                                                                    Claim 11; Page 1203-1206; 5507pp; English.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                          Leach M;
                                                     (CURA-) CURAGEN CORP.
                                                                                                                          WPI; 2000-602362/57.
N-PSDB; AAC75154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1532 AA;
                                                                                          Shimkets RA,
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1088 SGLTTSTEIEATTTSPTEA-----PSP-----AVSSGTDVTTEPTDTREQPTTLSTTSK 1136 1046 Ipvtdassistghatsihvtdassvstghatilihvtdassastghttsipvtdassvstg 1105 1166 assghatslpvtdassvstghatslpvtlpssassgdatslpvtslsslstghatplpvt 1225 986 EIEIVTTSSTKVLPPVVSSN-----TDLTSEPTNTREQPTTLSTTSNSITEDIT 1034 1226 slssastghatplpvtdtssvstghatsllvtdassvstg-hatplhvtdassvstgdtt 1284 1035 TSQPTGDNGDNTSSTNPVPTVATSTLAS-----ASEEDNKSGSHESASTSLKPSMGEN 1087 1285 plpvtspssastgdttplpvtdtssvstgdttpllvtdtssvstsh---atsl--pvtdt 1339 1137 TNSELVATTQATNENGGKSPSTDLTSSLTTG-----TSASTSANSEL-VTSGS-- 1183 1184 VTGGAV-----ASASNDQSHSTSVTNSNSIVSNTPQTTLSQQVTSSSPSTNTF1ASTY 1236 1106 dttplpvtdtssastgdttplhvtdassvstghatplhvtslssvstgdttplpvtspss 1165 892 -TSTVPTASTMSDSLSSTDGISATSSDNVS---KSGVSVTTETSVTTIQTTPNPLSS--- 944 945 ----SVTSL--TQLSSIPSVSESESKVTFTSNGDNQSGT------HDSQSTST 985 661 spmtdtktvttpgssftasghspseivpgdaptis-----aattfapaptg---- 706 165 IIREPPNHTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVTTEYWSQSFATTT 524 -----dghttg------apttalgatpsshdatl-----gpsggtslsktgaltlan 747 525 TVTAPPGGTDSVIIREPPNPTVTTTEYWSQSYATTTTVTAPPGGTDSVIIREPPNHTVTT 584 748 svvstpggpeg----amth 777 585 TEYWSQSYATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFATTTTVTGPPSGTDTV 644 778 thqaesteasgqtqtsepassgs----rttsagtatpsssgasgtt----psgseg1 826 645 ----IIREPPNP-----TVTTTEYWSQSYATTTTTAPPGETOTVLIREPPNHTVTTT 693 827 stsgettrfssnpsrdshttgsttellsas-ashgalpvstgmassiv---pgtfhptls 882 EYWSOSYATITIVTAPPGEIDTVLIREPPNHTVTTTEYWSOSYATTT-----TVTAPPGG 748 883 e----astagrptgqssptspsaspgetaaisr-magtgrtrtsrgsdtislasga 933 749 TDTVIIREPPNPTVTTEYWSQSFATTTTVTAPPGG--------TDTVIIYESMS 795 934 tdtfstvpptppsitssgltspq---tqthtlspsgsgktfttallsnatplpvtyassa 990 796 SSKISTSSN--DITSIIPSFSRPHYVNSTTSDLSTFESSSM--NTPTSISSDGMLLSSTT 851 852 L-VTESET-----TTELICSDGKECS------RLSSSSGIVTN-PDSNESSIV-- 891 105 SEWIGIITITITRINPIDSIDIVVVQVPLPNPIVSITEYWSQSFAITITVIAPPGGIDIV 464 AAW48299 standard; Protein; 1721 AA 401

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974 QSGTHDSQ------STSTEIEIVT-----TSSTKVLPPVVSSNTDLT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1010 SEPTNTREQPTTLS----TTSNSITEDITTSQPTGD-NGDNTSSTNPVPTVATS----T 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          995 inptnnntmdssfagaykyavsngiktdnvyglpvgeitglpkdpgsdipfnsttgelvd 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1060 LASASEEDNKSGSHESASTSLKPSMGENSGL---TTSTEIEATTTSPTEAPSPAVSSGTD 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1115 gttkpkpg1pvngggvvpdeeakdq----adkgkdglivpptnsin----kdpvtntqy 1165
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                                                                                                                                                                                                                                                                                                                                 519 vspygskdvslisapiqpselfnevycdtctakygalhsgyqtsadfvttttakpttttt 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             636 GPPSGTDTVIIREPPNPIVITIEYWSQSYATTITITAPPGETDTVLIREPPNHIVITIEY 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 696 WSQSYATTTTVTAPPGETDTVLIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVIIR 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          618 --tgkpttttttkvpg------kpplattttt---lkplvtttttkattttttv--- 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       idepipgsqaaqaadtsnlfpvqthkstglpidpmvglpfdpksgnlvhpytnqtmsgls 775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       893 edggi------ippevaaanadkfklsippsvpesipekdgkidsiselmydi 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940 esgrliggvskrpipgslagdlnpimktptqtdsvtgkpidpttglpfnpp----tghl 994
DSVIIREPPNPTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSYA 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    756 EPPNPTVTTTEYWSQSFATTTTVTAPPGG------TDTVIIYESMSSSKIST 801
                                                                 | : : | :|
459 thvrfrfkvkdvgntlsvrcrkgagklefpdrsldftippvaghnscs11vgvsgdgkih
                                                                                                                                                                                                                                                                                                                                                                                                       SSN------SPSRPH-YVNSTTSDLS
                                                                                                                                                                                                           581 TVTTTEYWSQSYATTTTV------TAPP-----TAPP-----
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                                                                                                                           558 TTTTVTAPPGGTDSVIIRE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 dsitglptdpysncp--fnpvtgnlvsrstgktipntyagvyrsnet----kttepsan 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 RWTG-YKNSD------AGSNGIVI----- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 tyagvyrsnetkttepsantnfllvdpkinaponsensfeggqifdmgskvyipytkovg 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 -----VATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTITTSYVGVTTS 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 MGFSSSNGDVAIDCSNIHIGITKG-LNDWNYPVSSESFSYTKTC-----TSNGIQI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                     Open reading frame; ORF; antigen; GP900; cryptosporidium; infection; antibody; proppylaxis; treatment; inhibition; retardation; decection; dagnosis; human; 3' region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of the GP900 antigen which may be used in the production of anti-Cryptosporidium antibodies. These can be used for the prophylaxis, treatment, inhibition or retardation of a Cryptosporidium infection in humans or in animals such as calves. They can also be used for the detection and diagnosis of related infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-Cryptosporidium antibody - used to develop products for detection, diagnosis, prophylaxis or treatment of Cryptosporidium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.5%; Score 488; DB 19; Length 1721; Best Local Similarity 22.5%; Pred. No. 6.5e-17; Matches 303; Conservative 128; Mismatches 469; Indels 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petersen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>-</del>:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; Pages 65-68; 89pp; English.
                                                                                Cryptosporidium parvum GP900 antigen
                                                                                                                                                                                                                                                 Location/Qualifiers
175..423
/note= "NINC domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leech J, Nelson RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0700651.
                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US14104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-159290/14.
N-PSDB; AAV20700, AAV20701.
                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
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                                     17-AUG-1998
                                                                                                                                                                                                                                                                                                                                      WO9806430-A1
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Domain
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AAB11727 standard; Protein; 1721 AA

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GP900; NINC isolate; glycoprotein; antibody; cryptosporidiosis; competitive inhibition; attachment; invasion; ligand binding; sporozoite; merozoite; diarrhoea; protozoacide.
                                                                                                                                                                                                                                                                                                                                      New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900
                                                          Portion of Cryptosporidium parvum NINC isolate GP900
                                                                                                                                                                                                     96US-0026062.
93US-0071880.
92US-0891301.
95US-0415751.
96US-0700651.
                                                                                                                                                                                   97US-0928361.
                                                                                                                                                                                                                                                                                                           WPI; 2000-422065/36.
N-PSDB; AAA61848, AAA61849.
                                     28-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                       Cryptosporidium parvum.
                                                                                                                                                                                                      13-SEP-1996;
01-JUN-1993;
29-MAY-1992;
                                                                                                                                                                                   12-SEP-1997;
                                                                                                                                          US6071518-A.
                                                                                                                                                              06-JUN-2000
                                                                                                                                                                                                                                                 14-AUG-1996;
                                                                                                                                                                                                                                                                                         Petersen C;
```

The invention relates to the GP900 glycoprotein of the protozoan Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion proteins comprising GP900 fragments. The invention also relates to the administration of GP900 refragments thereof to a host to elloit anti-capturation of GP900 or fragments thereof to a host to elloit anti-capture antibody production, and to a method of cryptosporidiosis treatment or prophylaxis comprising administration of anti-GP900 antibodies to an individual. Cryptosporidium parvum GP900 and GP900 fragments are able to competitively inhibit sporozoite or merozoite attachment or invasion, and are also useful for the generation of anti-GP900 antibodies. The antibodies also inhibit sporozoite or merozoite attachment/invasion and additionally inhibit the binding of GP900 injugands to GP900. GP900 proteins, fragments and antibodies may therefore be used to treat or cause of dlarrhoea in humans and causes life-threatening dlarrhoea in immunocompromised persons. Cryptosporidiosis can be contracted from contaminated municipal water supplies (e-g., public swimming pools). It is also a cause of dlasease in animals, resulting in financial losses in agriculture. GP900 fragments, fusion proteins and antibodies may also be used for the parasite in the environment. The present sequence Claim 2; Column 61-70; 59pp; English. Cryptosporidium parvum.

1721 AA; Sequence

8888888888888**%**8

Query Match

58; 1.5%; Score 488; DB 21; Length 1721; illarity 22.5%; Pred. No. 6.58-17; Conservative 128; Mismatches 469; Indels 448; Gaps 214 MGFSSSNGDVAIDCSNIHIGITKG-LNDWNYPVSSESFSYTKTC-----TSNGIQI 263 19 Inftsttgfttdtsmnwpvsitsgelkd---pnkqatisgsrscgwkqgysidsstgfrv 75 Best Local Similarity Matches 303; Conserva q ò

974 QSGTHDSQ------STSTEIEIVT-----TSSTKVLPPVVSSNTDLT 1009 1010 SEPTNTREQPTTLS----TTSNSITEDITTSQPTGD-NGDNTSSTNPVPTVATS---T 1059 264 ------KYONVPAGYRPFIDAYIS----ATDVNQYTLAYINDYTCAGSRLQSKPFTL 310 76 dsitglptdpysncp--fnpvtgnlvsrstgktipntyagvyrsnet----kttepsan 128 129 tyagvyrsnetkttepsantnfllvdpkinapcnsensfegggifdmgskvyipytkcvg 188 328 -----VATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTTTTTSYVGVTTS 377 378 YLTKTAPIGETATVIVDVPXHTTTTVTSEWTGTITTTTTTTTNPTDSIDTVVVQVPLPNPT 437 438 VSTTEYWSQSFATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFATTTTVTAPPGGT 497 498 DSVIIREPPNPTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSYA 557 360 ------ttttttttttttttttttttttttttttt 401 558 TTTTVTAPPGGTDSVIIRE-----PDNH 580 402 ttttttse---tesvikpdewcwlekngeceakgatyvgvigkdgriengmaftmipndd 458 459 thvrfrfkvkdvgntisvrcrkgagklefpdrsldftippvaghnscsiivgvsgdgkih 518 603 ----GGTDTVIIREP--PNH-----TVTTTEY------WSQSFAT-----TTTVT 635 519 vspygskdvslisapigpselfnevycdtctakygaihsgygtsadfvttttakpttttt 578 636 GPPSGTDTVIIREPPNPTVTTTEYWSQSYATTTTITAPPGETDTVLIREPPNHTVTTTEY 695 579 gapgqptttttgspskpttttt----tkatttttlnp-------11ttt-- 617 696 WSQSYATTTTVTAPPGETDTVLIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVIIR 755 662 ----ptttttt--krdemtttttplpdigdieitpipiekmldkytrmiydynsglllds 715 716 ndepipgsqaaqaadtsnlfpvqthkstglpidpmvglpfdpksgnlvhpytnqtmsgls 775 828 TFESSSMNTPTSISSD------GMLLSSTTLVTESETTTELICSDGKECSRLSSS 876 877 SGIVTNPDSNES--SIVTSTVPTASTM----SDSLSSTDGI-----SATSSDNV 919 833 agivsgisasesllsgksalidpatnmvvgefggllnpatgvmlpgflgpsegtgfspei 892 920 SKSGVSVTTETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSES----ESKVTFTSN--GDN 973 893 edggi-----ippevaaanadkfklsippsvpesipekdqkidsiselmydi 939 940 esgrliggvskrpipgslagdlnpimktptgtdsvtgkpidpttglpfnpp----tghl 994 618 --tgkpttttttkvpg------kpplattttt---lkplvtttttkatttttv--- 661 756 EPPNPTVTTTEYWSQSFATTTTVTAPPGG------TDTVIIYESMSSSKIST 801 802 SSN------DITSIIP---------SFSRPH-YVNSTTSDLS 827 776 vsylaakn--ltvdtdetyglpidtltgypldpvslipfnpetgelfdpisdelmn-gti 832 311 RWTG-YKNSD-----AGSNGIVI-----g qq g g οp a οp qq qq ò ò ò ò ò οy ò ò Ω ò ò ò ŏ QQ ò QΩ ò αg ò g δ QQ

arch completed: October 3, 2002, 15:32:14 b time: 366 sec THIS PAGE BLANK (USPTO)

APPLI APPLI

Sequence 5, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 7, A Sequence 7, A Sequence 4, A Sequence 4, A Sequence 2, A Sequence 3, A Se

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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08325267A Patent No. 5585271 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      ULT 1
08-325-267A-2
Search time 16.32 Seconds (without alignments) 1885.800 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Appil Sequence 2, Appil Sequence 5, Appil Sequence 6, Appil Sequence 7, Appil Sequence 7, Appil Sequence 7, Appil Sequence 2, Appil Sequence 2, Appil Sequence 40, Appil Sequence 40, Appil Sequence 40, Appil Sequence 40, Appil Sequence 2, Appil Sequence 3, Appil Sequence 4, Appil Sequence 4, Appil Sequence 6, Appil Sequence
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                                                                                                                                                    US-09-715-876-8
6495
1 MLQOFTLLFLYLSIASAKTI.....SIIQHSTWLYGLITLLSLFI 1260
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1. /cgn2_6/ptcdatu2/21aa/5A_COMB.pep:*

2. /cgn2_6/ptcdatu2/21aa/5B_COMB.pep:*

3. /cgn2_6/ptcdatu2/21aa/6A_COMB.pep:*

4. /cgn2_6/ptcdatu2/21aa/6B_COMB.pep:*

5. /cgn2_6/ptcdatu2/21aa/ptcTUS_COMB.pep:*

5. /cgn2_6/ptcdatu2/21aa/pcTUS_COMB.pep:*

5. /cgn2_6/ptcdatu2/21aa/pcTUS_COMB.pep:*

5. /cgn2_6/ptcdatu2/21aa/pcTUS_COMB.pep:*
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US. 08-928-318-6
US-08-228-3618-5
US-08-228-3618-5
US-08-225-267A-4
US-08-046-385-5
US-08-046-385-5
US-08-045-555-5
US-08-05-555-5
US-08-05-555-5
US-08-05-556-4
US-08-05-96-4
US-08-99-644-40
US-08-944-438A-40
US-08-944-438A-40
US-08-944-438A-40
US-08-944-438A-40
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US-08-944-868A-40
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S-08-928-3618-27
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3-09-165-239A-4
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PCT-US95-10661A-6
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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917 FISTSTEMTTVTGTNGVPTDETVIVIRTPTSEGLISTTTEPWTGTFTSTSTEVTTITGTN 976 DATA FILING DATE: 04-JAN-CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: NUMBER OF SEQUENCES: CURRENT APPLICATION GENERAL INFORMATION: APPLICANT: KLIS, F 08-362-525-22 COUNTRY: δý ò õ ò Query Match 14.5%; Score 940; DB 1; Length 1537; Best Local Similarity 26.0%; Pred. No. 3.5e-46; Matches 417; Conservative 244; Mismatches 523; Indels 418; Gaps 69 KLGSVGGQTDISIDYNIPCVSSSGTFPCPQEDSYGNWGCKGMGACSNSQGIAYWSTDLFG 128 129 FYTTPTNV-TLEMTGYFLPPQTGSYTFKFATVDDSAILSVGGATAFNCCAQQQPPITSTN 187 LTADGVK-----YATCQFYSGEEFTTFSTLTCTVNDALKSSIKAFGT----VTLP 131 188 FTIDGIKPWGGSLPPNIEGTVYMYAGYYYPM-----KVVVYSNAVSWGTLPISVTLP 238 IAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTV-DPSAYLYASRVM 190 -----DGTTVSDDFEG------YVYSFDD------DLSQSNCTVPDPSNYA-VSTTT 277 191 PSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESF 250 278 TITEPWIGTFISTSTEMTIVIGINGVPIDETVIVIRIPITASTIITITEPWNSTFISTST 337 251 SYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTL 310 338 ELTIVICINGVRIDETII-----VIRTPITATITITIEPWNSTFISTSTEL----- 384 311 RWTGYKNSDAGSNGI---VIVATTRTVTDSTTAVTTL-PFNPSVDKTKT------ 355 356 -----IEILQPIPTTTTT-----SYVGVTTSYLTKTA----PIGETATVIVDVPYH 398 439 PIDETIIVIRTPITATTAMTITQPWDDIFTSTSTEMTIVIGINGLPIDET-IIVIRTPIT 497 399 TTT--TVTSEWIGTIT-----TTTTRIN--PTDSIDTVVVQVPLPNPT-VSTTEYWSQS 447 448 FATT----TTVTAPPG-GTD--TVIIREPPNHT--VTTTEYWSQSFATT----TTVTAPP 494 557 FTSTSTEMTTVTGTNGLPTDETIIVIRTPTTATTAITTEPWNSTFTSTSTELTTVTGTN 616 495 G-GTDS--VIIREPPNPT--VTTTEYWSQSFATT----TTVTAPPG-GTDS--VIIREPP 542 543 NPT--VTTTEYWSQSYATT----TTVTAPPG-GTDS--VIIREPPNHT--VTTTEYWSQS 591 677 TATTAMITIQPWNDIFISISTEMIIVIGINGLPIDETIIVIRIPITATTAMITIQPWNDI 736 592 YATT----TTVTAPPG-GTD--TVIIREPPNHTV--TTTEYWSOSFATT----TTVT--- 635 737 FISTSTEMITVICINGVPIDETVIVIRIPISEGLISTTIEPWIGTFISTEMITVIGIN 796 636 GPPSGTDTVIIREPPNP--TVTTTEYWSQSYATT----TTITAP---PGETDTVLIREPP 686 797 GOPTDETVIVIRTPISEGLVTTTTEPWTGTFTSTSTEMTTITGTNGVPTDETVIVIRTPT 856 687 NHTV--TTTEYWSQSYATT----TTVTAPPGE-TD--TVLIREPPNHTV--TTTEYWSQS 735 857 SEGLISTTTEPWTCTFTSTSTEMTTITGTNGQPTDETVIVIRTPTSEGLISTTTEPWTGT 916 2 LOOFTLLFLYLSIASAKT-----ITGVFDSF-----NSLTWSNAANYAF----- 40 10 LAVFTLLAL-TSVASGATEACLPAGORKSGMNINFYQYSLKDSSTYSNAAYMAYGYASKT 68 41 ------NAVLGWSLD--G 58 59 TSANPGDTFTLNM----TSVD 85 US-08-325-267A-2

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APPLICANN: KLIS, FRANCISCUS M.
APPLICANY: SCHRUDER, MARTER P.
APPLICANY: TOSCHEM, HOLGER Y.
APPLICANT: VERRIPS, CORNELIS T.
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                     1037 SEGLVITITEPWIGIFISTSTEMSTVTGINGLPIDETVIVVKTPTIAISSSLSSSSGQI 1096
                                                                                                                                                                                                                                                                                          988 EIVTTSST-----KVLPPVVSSNTDLTSEPTNTREQPTTLSTTS-----NSITEDITT 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1206 PLVTSATTSQETASSLPPATT----TYTSEQTTLVTVTSCESHVCTESISPAIVS 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1036 SQPTGDNGDNTSSTN--PVPTVATSTLASASEEDNKSGSHESASTSLKPSMGENSGLTTS 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1257 TATVTVSGVTTEYTTWCPISTTETTKQTKGTTEQTTETTKQTTVVTISSCESDVCSKTAS 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1094 TELEGATTTSPTEAPSPAVSSGTDVTTEPTDTREQPTTLSTT-----SKTNSELVATT- 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1317 PAIVSTSTATINGVTTEYTTWCPIST--TESRQOTTLVTVTSCESGVCSETASPAIVSTA 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1435 ETKTVVTSSLSRSNHAETQTASATDVIGHSSSVVSVSETGNTKSLTSSGLSTMSQQPRST 1494
                                 1189 -------VASASNDQSHSTSV----TNSNSIVSNTPQTTLSQQVTSS 1224
786 -----DIVIIYESMSSSKI------STJSNDITSIIPSFSRP------ 816
                                                                                                                        817 --HYVNSTTSD-LSTFESSSMNTPTSISSDGMLLSSTTLVTESETT----TELICSDGKE 869
                                                                                                                                                                                                                                                    870 CSRLSSSSGIVTNP--DSNESSIVTSTVPTASTMSDSLSSTDGISATSSDNVSKSGVSVT 927
                                                                                                                                                                                                                                                                                                                                                                                 928 TETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSESESKVTFTSNGDNQSGTHDSQSTSTEI 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1225 SP----STNTFIASTYDGSGSIIQHSTWLYGLITLLSLFI 1260
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PatentIn Release #1.0, Version #1.25
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ADDRESSEE: CUSHMAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 1100 New York Avenue, N.W. Washington
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04-JAN-1995
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Patent No. 6027910
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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53 TYSNAAYMAYGYASKTKLGSVGGQTDISIDYNIPCVSSSGTFPCPQEDSYGNWGCKGMGA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EYWSQS-FATTTVTAPPGGTDSVIIREPPNPTVTTTEY------WSQSFA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TT-TTVTAPPGGTDSVLIREPPNPTVTTTEXWSQSYATTTTVTAPPGGTDSVLIREPPNH 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 TVDDSAILSVGGATAFNCCAQQQPPITSTNF-----TIDGIKPWGGS------LPPNI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   581 TVTTTEYWSOSY------DTVI 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 EGTVYMYAGYYYPMKVVYSNAVSWGTLPISVTLPDGTTVSDDFEGYVYSFDDDLSQSNCT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEYWSQSYATT ----TIITAPPGE-TD--TVLIREPPNHTV--TTTEYWSQSYATT---- 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610 IREPPNH----TVTTTEYWSOSFATT----TTVTGP---PSGTDTVIIREPPNPTV--TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
7.9%; Score 516; DB 3; Length 894;
Best Local Similarity 26.3%; Pred. No. 4.5e-22;
Matches 251; Conservative 126; Mismatches 310; Indels 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437 TVSTTEYWSQSFATTTTVTAPPGGTDTVIIREPPNHTVTTT----------
                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-08-971-692-15
US-08-971-692-15
Sequence 15, Application US/08971692
Patent No. 614147
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522 TT-TTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSYATTTTVTAPPGGTDSVIIREPPNH 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 -----EVWSQS-FATTIVTAPPGGTDSVIIREPPNPTVTTTEY------WSQSFA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 CSNSQGIAYWSTDLFGFYTT-------PTNVTLEMTGYFLPPQTGSYTFKFA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVDDSALLSVGGATAFNCCAQQQPPITSTNF-----TIDGIKPWGGS-----LPPNI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   581 TVTTTEYWSQSY------DTVI 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 EGTVYNYAGYYYPMKVVYSNAVSMGTLPISVTLPDGTTVSDDFEGYVXSFDDDLSQSNCT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610 IREPPNH----TVTTTEYMSQSFATT----TTVTGP---PSGTDTVIIREPPNPTV--TT 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 VPDPSNYAVSTTTTTEPWIGTFTSTSTEWITVTGTNGVPTDETVIVIRIPTSEGLISTT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              657 TEYWSQSYATT----TTITAPPGE-TD--TVLIREPPNHTV--TTTEYWSQSYATT---- 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       704 TIVTAPPGETDTVLIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVIIREPPNP--T 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTVTGTNG------OPTDETV------IVIRTPTSEGLV 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              762 VITTEYWSOSFATTTTVTAPPGGT-----DTVIIYE----SMSSSKISTSSNDITSIIP 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    812 SFSR----PHYVNSTTSDLSTFESSSMNTPTSISSDGMLLSSTTLVTESETTTELICSDG 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             868 KECSRLSSSSGIVTNPDSNESSIVTSTVPTASTMSDSLSSTDGISATSSDNVSKSGVSVT 927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.9%; Score 516; DB 3; Length 894;
Best Local Similarity 26.3%; Pred. No. 4.5e.22;
Matches 251; Conservative 126; Mismatches 310; Indels 266;
      PILLON LOWER TO BE THE TELLING DATE: BE SUB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 9203899.7
FILLING DATE: I 4-DEC.1993
FILLING DATE: I 7-DEC.1993
APPLICATION NUMBER: PCTEP93/01763
FILLING DATE: I 7-DL-1993
APPLICATION NUMBER: PAUL N.
RESISTRATION NUMBER: 16,73
RECISTRATION NUMBER: 23,73
TELEPHONE: (202) 861-3000
TELEFAX: (202) 861-3000
TELEFAX: (5102) 82-0940
TELEFX: (5102) 84-0940
APPLICATION NUMBER: EP 92202080.5
FILING DATE: 08-JUL-1992
                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-362-525-22
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DEPLACANT:

TITLE OF INVENTION: Immobilized proteins with specific binding title OF INVENTION: opacities and their use in processes and products. COMPUTER READABLE FORM:

OMPUTER READABLE FORM:

MUMBER OF SEQUENCES: 40
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOG/MS-DOS
CURRENE: PAPELCATION NATA:

APPLICATION NUMBER: US/08/971,692
FILING DATE:
FILING DATE:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acids
TYPE: amino acid

TYPE: amino acid

TYPE: amino acid 1048 STNPVPTVATSTLASASEED--NKSGSHESASTSLKPSMCENSGLTT----STEIEATT 1100 EIVITSSTKVLPPVVSSNTDLTSEPTNTREQPTTLSTTSNSITEDITTSQPTGDNGDNTS 1047 1101 TSPT------EAPSPA-VSSGTD-----VTTEPTDTREQPTTLSTTSKTNSELVAT 1144 1145 TOATNENGGKSPSTDLTSSLTTGTSASTSANSELVTSGSVTGG----AVASASNDQSHS 1199 614 HVCTES---ISPAIVSTATVIVSGVTTEXTTWCPISTTE-----TTKOTKGTT-EQTT 662 663 ETTKQTTVVT---ISSCESDVCSKTASPAIVSTSTATINGVTTEVTTMCPISTTESRQOT 719 780 T--TNTLAAETTTNTVAAETITNTGA---AETKTVVTSSLSRSNHAETGTASATDVIGHS 834 1200 TSV----TNSNSIVSNTPQTTLSQQVTSSSP----STNTFIASTYDGSGS 1241 :|| | : :::: :||| |: 835 SSVVSVSETGNTKSLTSSGLSTMSQOPRSTPASSMVGYSTASLEISTYAGSAT 887

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ATTELLA SECULATION OF THE SECURATION OF THE SECU	
	STATE: CA COUNTRY: CA COUNTRY: CA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: TBM PC COMPATIBLE COMPUTER: PACEDOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE PACEDICATION DATA: RPLICATION NUMBER: US/08/928,361B FTLIC DATE: 12-SEP-1997 CLASSIPICATION DATA: PRIOR APPLICATION DATA:

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PP-VVSSNTD--LISEPINTREQPTILSTISNSITE---DITISQPIGD-----NGDNT 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLLSQKSALIDPATNMVVGEFGGLLNPATGVMIPGFLGPSEQTQFSPEIE-----DGGII 898
                                                                                                                                                                                                                                                      124 IDTVVVQVPLPNPTVSTTEYMSQSFATTTTVTAPPGGTDTVIIREPPNHTVTTTEYMSQS 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTDIVIIREPPNHTVTTTEYWSQSFATTTTVTGPPSGTDTVIIREPPNPTVTTTEYWSQS 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S----KVTFTSNGDNQ-------SGTHDSQSTSTELELVTTSSTKVL 998
                                                                                                                                                           401 -ATTTTTTSETESVIKPDEWCWLEKNGECEAKGATYVGVIGKDGRIENGMAFTMIPNDDT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          705 TVTAPPGETDTVLIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVIIREPPNPTVTT 764
52 TISGSRS------CGWK-----QGYSIDSSTGFRVDSITGLPTDPYSNCPFNPVTG
                                                            352 KTKTIEILQPIPTT-----TITT----SYVGVTTSYLTKTA-PIGETATVIVD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        765 TEYWSQSFATTTTVTAPPGGTDTVIIYESMSSSKISTSSNDITSIIPSFSRPHYVNSTTS
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                                                                                                           NLVSRSTGKTIPNTYAGVYRSNETKTTEPSANTYAGVYRSNETKTTEPSANTNFLLVDPK
                                                                                                                                                                                            484 FATTTTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPN
                                                                                                                                                                                                                                                                                                                                                                                           544 PTVTTTEYWSQSYATTTTVTAPPGGTDSVIIREPPNHTVTTTEYWSQSYATTTTVTAPPG
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APPLICANT: DETERBEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPLOSPOCIATION PARTITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPLOSPOCIATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1055 PSTGRPINNSTAGIVSGKPGLPPIEDENGNLFDPSTNLPIDGNNQLVNPETNSTVSGSTS 1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1115 GTTKPKPGIPVNGGGVVPDEEAKDQ-----ADKGKDGLIVPPTNSIN----KDPVTNTQY 1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1166 SNTTG----NINPE---TGKVIPGSLPGSLNYPSF------NTPQQT--DEIT 1204
                                                                                                                                                                                                                                                                                                                                                                                           QSCTHDSQ------STSTEIEIVT-----TSSTKVLPPVVSSNTDLT 1009
                                                    776 VSYLAAKN--LIVDTDETYGLPIDTLTGYPLDPVSLIPFNPETGELFDPISDEIMN-GTI 832
                                                                                                                                                                                                    SGIVINPDSNES--SIVTSTVPTASTM----SDSLSSTDGI-----SATSSDNV 919
                                                                                                                                                                                                                                           833 AGIVSGISASESLLSQKSALIDPATNMVVGEFGGLLNPATGVMIPGFLGPSEQTQFSPEI 892
                                                                                                                                                                                                                                                                                             920 SKSGVSVTTETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSES----ESKVTFTSN--GDN 973
                                                                                                                                                                                                                                                                                                                                 940 ESGRLIGQVSKRPIPGSIAGDLNPIMKTPTQTDSVTGKPIDPTTGLPFNPP-----TGHL 994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1223 SSSPSTNTFIASTYDGS-GSIIQHSTWL 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08700651B Patent No. 6015882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-08-700-651-5
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-08-700-651-5
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297 TCAGSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTT-----LPFNPSVD 351

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QY         247         SESFSYTKTCTSNCIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSK         306           Db         179	395 VPYHITTTUTSEWIGIITTTTTRINPIDSIDIVVVQVPLENPTVSTTEYWSOS	OY 508 PTUTITEXMSOSFATITIVIAPPGGIDSVIIREPPNPTVITIEXMSOSYATITIVIAPPG 567  Db 402 TITITITITITITITITITITITITITITITITITITI	OY 628 FATTTTVTGPPSGTDTVIIREP	632 GKIHVSPYGSKÖVSLÍSAPIQPCELENEVÝCDŤCTAKYGAIHSGYQTSADFVŢŦŢŢ 708 APPGETDTVLIREPPNHTVTTEYWSOSYATŤTYTAPPGGTDTVIIREPPNHTVTTTY 688 AKPŢTŢŢGAPGQPTŢTŢGSPSKPŢŢŢŢŢŢKATŢŢŢŢĪNPIIŢŢŢŢŢNPIIŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢ	Db 784 TTKRDEMTTTTPLPDIGDIETTPIPIEKMLDKYTRMIYDYNSGLLLDSNDEPIPGSQAG 843  Qy 872 RLSSSGIVTNPDSNESSIV-TSTVPTASTMSDSLSSTDGISA 913  :::	Oy 963 SKVTPTSNGDNOSGTHDSOSTSTEIBIUTTSSTKVL 998    :
SLPPI 1078 1153 SEAKD 1138 ASND 1195 SSLNY 1191	NTPQQTDEITGKPVDTVTGLPYDPSTGEIIDPATKL 1230  Splication US/08928361B AMATON:	PETERSEN, CARCHIDES, POLYPEPTIDES, GLYCOPROTEINS, NVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, NVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS NVENTION: FOR TREATMENT AND DEFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SEQUENCES: 30 SEQUENCES: 30 SECUENCESS: 30	snue, Suite 6 sk lb le 5/KS-DOS sase #1.0, Version #1.30	COATON NUMBER: US/08/928,361B ARION: ARION: COATON DATA: COATON UNMBER: 06 60 00 00 00 00 00 00 00 00 00 00 00	TELEPAX: 650-324-1678   DB     INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERICS:	Ouery Match  17.5%; Score 487; DB 3; Length 1837;  Best Local Similarity 22.8%; Pred; No. 5.7e-20;  Matches 316; Conservative 146; Mismatches 487; Indels 440; Gaps 61;  136 VGGTGSSTDLEDSKCFTAGTNTVTEN-DGDRISSIDVEFEKSTVDP-SAYLYASR 188  136 IDSTGKKFSPYTGKHADASTTSSAYSAPFELDVS-CVPIEDNTRRAVDEVSLMLFDNSTG 127  189 VMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVS 246  1189 VMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVS 246  128 VMYDPNTNSILEGSIAGIRSESCIVSELNFTSTTGFTTDTSMNMPVSITSG

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545 TVTTTEYWSQSYATTTTVTAPPGGTDSVIIREPPNHTVTTT-
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1105 EAPSPAVSSG--TD-----VITEPIDIREOPTILSTISKINSELV--ATTOAIN----- 1149
                                                                                                                                                                                                                                                                 1184 VTGGAVA-SASNDQSHSTS----VTNSNSIVSNTPQTTLSQQVTSSSPSTNTFIASTYDG 1238
                                                               1126 GAYKYAVSNGIKTDNVYGLPVDEITGLPKDPVSDIPFNSTTGELVDPSTGKPINNYTAGI 1185
                                                                                                                                  ------ENGGK-SPSTDL-----TSSLTTG-TSASTSANSELVTSGS 1183
                                                                                                                                                                                                                                                                                                                            1245 --GGVVPDEEAKDQADKGKDGLIVPPINSI-------NKDPVINIQYSNT--- 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                     1186 VSGKRGLPPIEDENGNLFDPSTKLPIDGNNQLVNPETNSTVSGSTSGSTKPKPGIPVNG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TAKATA, JUNJI
APPLICANT: TAKATA, YOSHHIRO
APPLICANT: TAKATA, YOSHHIRO
APPLICANT: PENTILA, MESHIRO
APPLICANT: ONDELA, MAJA-LEENA
APPLICANT: ONERTICA, MAJA-LEENA
APPLICANT: ONERTICA, MAJA-LEENA
APPLICANT: KERAKEN, SIRKKA
APPLICANT: KERAKEN, SIRKKA
APLICANT: CONTENTION: CONTAINING THEM
NUMBER OF SECURORES: TOORRESPONDENCE ADDRESS:
ADDRESSE: ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
7.2%; Score 468.5; DB 1;
Best Local Similarity 26.3%; Pred. No. 2.3e-19;
Matches 231; Conservative 120; Manatches 297,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION UNMBER: US/08/35,267A
FILING DATE: 18 NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER: JP PCT/JP94/00290
FILING DATE: 24 FEB-1994
PROR APPLICATION NUMBER: JP 3871/1993
FILING DATE: 26 FEB-1993
ATTORNEY/AGENT INCORMATION:
NAME: OBLON, NORMAN ERERRENCE/POCKET UNMBER: 24,618
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $-08-325-267A-4
$-08-325-267A-4
|Sequence 4. Application US/08325267A
Patent No. 54-55271
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 703-413-220
TELEPAX: 703-413-220
TELEPAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 862 maino acids
TYPE: amino acids
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1286 TGNIINPET 1294
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1023 STISNSITEDITISOPTGDNGDNTSSTNPVPTVATSTLASASEED--NKSGSHESASTSL 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .081 KPSMGENSGLTT----STEIEATTTSPT-----EAPSPA-VSSGTD----VTT 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPTDTREQPTTLSTTSKTNSELVATTQATNENGGKSPSTDLTSSLTTGTSASTSANSELV 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     695 YWSQSYATT----TTVTAP---PGETDTVLIREPPNHT--VTTTEYWSQSYATT----TT 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                          742 VTAPPG-GTD--TVIIREPPNP--TVTTTEYWSQSFATTTTVTAPPGGT-----DTVII 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                843 DGMLLSSTTLVTESETTTELICSDGKECSRLSSSSGIVTNPDSNESSIVTSTVPTASTMS 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSESE 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       765 VISSLSRSNHAETQTASATDVIGHSSSVVSVSETGNTKSLTSSGLSTMSQQPRSTPASSM 824
53 TYSNAAYMAYGYASKTKLGSVGGOTDISIDYNIPCVSSSGTFPCPQEDSYGNWGCKGMGA 112
                                                                                                                     113 CSNSQGIAYWSTDLFGFYTTPTNVTLEMTGYFLPPQTGSYTFKFATVDDSAILSVGGATA 172
                                                                                                                                                                                                                                    173 FNCCAQQQPPITSTNFTIDGIKPMGGSL-----PPNIEGTVYMYAGYYYPMKVVYSN 224
                                                                                                                                                                                                                                                                                                                                                          225 AVSWG---TLPISVTLPDGTTVSDDFEGYVYSFDDDLSOSNCTVPDPSNYAVSTTTTTE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           710 YPTWRPQTANEESVSSKMNSATGETT--TNTLAAETTINTVAAETITNTGA---AETKTV
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                                                                                                                                                                               611 -----REPP----NHTVTTTEYWSQSFATTTTVTGPPSGTDTVIIRE----PPNPTVTT
                                                                                                                                                                                                                                                                                                 657 TEYWSQSYATTTTITAPPGET----TVTTTE
                                                            -----EYWSOS----YATTTTVT-----APPGGT------DTVII----
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US-00-046-585-5
US-00-046-585-5
PAPLICALION US/08046585
PAPLICANT:
APPLICANT: Lemarco, Kelly
APPLICANT: Wilson, Angus
APPLICANT: Winship
TITLE OF INVENTION: A NOVEL EXARVOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: A NOVEL EXARVOTIC TRANSCRIPTION PROTEIN:
UNDBER OF SEQUENCES: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKSSIKAFGTVTLP 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAYLYASRVMP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I-ITVHKSGTVTVAQQAQVVTTVVGGVT----KTITL-----VKSPISVPGGSALIS 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFS 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLGKVMSVV---QTKPVQTSAVTG-QASTGPVT-----QIIQTKG-----7TKPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PLPAG----TILKLVTSADGKPTTITTTQASGAG-----TKPTIL- 751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTITTSYVGVTTSYLT----------KTAPIGETATVIVDVPYHTTTVT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEWTGTITTTTTTTTTPDSIDTVVVQVPLPNPTVSTTEYWSQSFATTTTVTAPPGGTDTV 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PVTVSAVKP--AVTTLVVKGTTGVTTLGTVT-----GTVSTSLAGAGGHST- 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 IASAKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAV-LGWSLDGTSA-NPGDTFTLNM 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 6.2%; Score 404.5; DB 1; Length 2035; Best Local Similarity 21.9%; Pred. No. 3.78-15; Matches 319; Conservative 165; Mismatches 506; Indels 467; Matches 506; Indels 467; Mat
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
CITY: San Francisco
CITY: SAN FRANCISCO
COUNTY: USA
ZIP: 94111-4187
                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/046,585
FILING DATE: 12-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RIChard A
REGISTRATION NUMBER: 36,67
REFERENCE/DOCKET NUMBER: A-57503-1/RAO
FELECOMMUNICATION INFORMATION:
TELEPHONIC ATION INFORMATION:
TELEPHONIC A15, 398-3249
TELEFAX: (415, 398-3249
TELEFAX: (415, 399-3249
TELEFAX: (415, 399-3249
TELEFAX: 210,2799
INFORMATION FOR SEQ. ID NO; 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino acids
TYPE: amino acid
STRANDENNESS: single
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MOLECULE TYPE: pep
US-08-046-585-5
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                                                                937 TLTAAGGLTTPTITMQPVSQPT-----QVTLITAPSG-----VEAQPVHDLP 978
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Patent No. 5585239
GENERAL INFORMATION:
APPLICANT: Lamarco, Kelly
APPLICANT: Wilson, Angus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 590 PATVKVASSPVMV----ATNTSTRP 631
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APPLICANT: Herr, Winship
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
NUMBER OF SEQUENCES: 15
CORRESPONDERS: 165
CONDERSESEE FLERK, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: LOA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
COMPUTER: BATELICATION DATA:
COMPUTER READABLE TORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
COURTRY: AFEB-1995
CLISSIFICATION WIMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
RECEPENA: 010 277299
TELECOMMUNICATION INPERM: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/OCKET NUMBER: 36,627
RELEPRA: 910 277299
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 anino acids
STRANDEDNESS: single
TOPOLOGY: 11near
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US-08-393-703-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                537 IGSSPQMSGM----AALAAAAATQKIPPSSAPTVLSVPAGTTIVKTMAVTPG---TTTL 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 IAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAYLYASRVMP 191
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GENERAL INFORMATION:
APPLICANT: Handle
APPLICANT: Hilson, Angus
APPLICANT: Hilson, Angus
APPLICANT: Her, Winship
TITLE OF INVEWTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVEWTION: HOST CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: 15
CORRESPONDENCE ADDRESS: 15
CORRESPONDENCE ADDRESS: 16
CORRESPONDENCE ADDRESS: 16
CORRESPONDENCE ADDRESS
STATE: CA
COMPRY: USA
COMPRY: USA
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CORRESPONDENCE: PATON DATA:
APPLICATION NUMBER: PCT/US93/11721
FILING DATE: 03 DEC-1993
CURRENT BATES
CORRESPONDENCES: DATES TO COMPATIBLE
CORRESPONDENCES: DATES TO COMPATIBLE COMPATIBLE
CORRESPONDENCES: DATES TO COMPATIBLE COMPAT
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NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-57503-1/RAO
FELEPHONE: (415) 781-1999
FELEFAX: (415) 398-3249
ITELERX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENTH: 2035 anino acids
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STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11721-5
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qa		:
Qy	465	PPGGTDSVIIREPPNPTVTTTEYWSQSE
qa	903	
Qy	525	SVI
qa	937	SQPTVEAQF
Qy	583	TITEYWSQSYATTIVTAPPGGIDIVIIREPPNHTVITTEYWSQSFAT 630
qa	979	ATVIIADSGQGDVQPGTVTLVCSNPPCETHETGTT
Qy	631	TTTVTGPPSGTIREPPNPTVTTEXWSGSY 664
qa	1031	TTVVANLGGHPQPTQVQFVCDRQEAAASLVTSTVGQQNGSVVRVCSNPPCETHETGTTNT 1090
Qy	999	
qa	1001	SNMAGQHGCSNPPCETHETGTTNTATTAMSSVGANHQRDARRACAAGTPAVIRI
οy	069	VITTEYWS
qa	1151	KSQCQTRQTSATSTTMTVMATGAPCSAGPLLGPSMAREPGGF
ογ	720	EPPAHTVTTEYWSQSYATTT 740
q	1211	LAPLSSKVRLSSPSIKDLPAGRHSHAVSTAAMTRSSVGAGEPRMAPVCESLQGGSPSTTV 1270
γo	741	TUTAPPGGTDTVIIREPPNPTVTTTEYWSQSFATTTTVTAPPGGTDTVIIYESMS 795
qa	1271	LEALLCPSATVTQVCSNPPCETHETGTTNTATTSNAGSAQR
Qy	196	SSKISTSSNDITSIIPSFSRPHYVNSTTSDLSTFE-SSSMNTPTSISS 842
qa	1324	GGQQPPAGRPCETHQTTSTGTTMSVSVGALLPDATS
QY	843	FTELICSDGKECSRLSSSGIVT
qa	1384	PFPTQRVCSNPF
٥y	889	SIVTSTVPTASTMSDSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLS 943
qa	1427	TGTTHTATTVTSNMSSNQDPPPAASDQGEVESTQGDSVNITSSSAITTTVSSTLT 1481
ρ	944	SSVTSLTQLSSIPSVSESESKVTFTSNGDNQSGTHDSQSTSTEIEIVTTSSTK 996
qa	1482	RAVITVIQSIPVEGESVEPPEELQVSFGFRQQLFPRQLLQSASTALMGESAEVLSASGTP 1541
Qy	266	TOLISEPTWIREQPTILSTISONSITEDITISOPTGDNGDNISSINPVPI
qa	1542	SAGSAVVATVVVQP
οy	1057	DNKSGSHESASTSLKPSMG
qa	1581	DELMAEAQAGTTTLMVTG
Oy	1114	GTDVTTEPTDTREQPTTLSTTSKTNSELVATTQATNENGGKSPSTDLTSSLTT 1166
qq	1638	TQAELGHLSAEGQEGQATTI
ΟY	1167	GTSASTSANSELVTSGSVTGGAVASASNDQSHSTSVTNSNSIVSNTPQTT 1216
qa	1689	PTEALAPADSLNDPALES
δλ	121	LSQOVTSSSPSTNTFIA
4	1747	

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169 V---VNF----DPAAFTENVFHSGRSTGYGSFESYHLGMYCPNGYFLGGTEKIDYDSSN 220
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ZIP: 10036/2711
COMPUTER REACABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM COMPALIADLE
OPERATING SYEPHE, DOS
SOFTWARE: FRASISEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,774
FILING DATE: 15-7AN-1997
CONSTRICTION OF STAN-1997
CONSTRUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LOUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-
TELEPHONE: 212-90-990
TELEPHONE: 212-90-990
TELEPRAX: 212-869-8864
TELEFAX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08783774 Patent No. 6054130 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 907 amino acids
amino acid
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US-08-783-774-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: N
STATE:
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                                                                                                                                    APPLICANT: KLIS, FRANCISCUS M.
APPLICANT: SCHEEDUBE, MARTEN P.
APPLICANT: SCHEEDUBE, MARTEN P.
APPLICANT: TOSCHEA, HOLSER Y.
APPLICANT: VERRIPS, CORNELIS T.
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 L-DGTSANPGDTFTLNMPCVFK---YTTSQTSVDLTADGVKYATCQFYSGE----EFTT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISIDVEFEKSTVDPSAY---LYASRVMPSLNKYTTLFVAPQCENGYTSG---TWGFSSSN 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 FTLLFLYL---SIASAKTITGVFDSFNSLTWSN-----AANYAFKGPGYPTWNAVLGWS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3918

COMPUTER READABLE PORM:
MEDIUM TYPE: PIOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PARCHINE PC-DOS/MS-TOOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLICATION WINBER: US/08/362,525
FILLIG DATE: 04.354
CLASSIFICATION: 435
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1100 New York Avenue, N.W.
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APPLICATION DATA:
FILING DATE: 08 JUL-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 14 -DEC-1992
PRIOR APPLICATION NUMBER: EP 92203899.7
PILING DATE: 14 -DEC-1992
                                                   Sequence 2, Application US/08362525
Patent No. 6027910
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
STATE: D. C.
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STREET: 110
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341 TIDLTSINISAYSTGSISTV ----ETGNRTTSEVISHVVTTSTKLSPTATTSLTIAQTSI 396
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221 GDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKY-QNVPAGYRPFIDAY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 TRTVTD-----STTAVTTLPFNPSVDKTKTIEILQPIPTTTITTSYVGVTTSYLTKTAP 384
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APPLICANT: Space, Richard
APPLICANT: Jackman, Minthrop
TITLE OF INVENTION: NON-SPLICING VARIANTS OF
TITLE OF INVENTION: GP350/220
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
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1061 ASASEEDNKSGSHESASTSLKPSMGENSGLTTSTEIEATT-TSPTEAPSPAVSSGTDVTT 1119
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CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
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MOLECULE TYPE:
PCT-US95-04611A-19
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PCT-US95-04611A-19
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                                                                                                                                                                                                                                                                       103 ALTM-------VSKKLPINVTTGEEQ---QVSLES-------VDVYFQDV-- 135
                                                                                                                                                                                                                                                                                                                                                                                                         378 NI------SGAFASNRTFDITVSGLGT-----APKTLIITRT----- 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PN-----ATGPTVGETSPQANAT------NHTLGG---TSPTPVVTSQ--PKNATS 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 TAGTN-TVTFNDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYT 210
                                                                                                                                                                                                                                              211 SGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQNVPA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVVQVPLPNPTVSTTEYWSQSFATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFAT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               593 ATTITVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFATTTTVTGPPSGTDTVIIREPP-- 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 -NPTVTTTEYWSQSYATTTT----ITAPPGETDTVLIREPPNHTVTTTEYWSQSYATTTT 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 TGPTVSTADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMT-----SSTSP 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             885 SNESSIVTSTVPTASTMSDSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLSS 944
                                                                                                                                              Gaps
                                                                                                                                                                                                         43 TADVNVTINFDVGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENATNLFLLELLGAGEL 102
                                                                                                                                                                                                                                                                                                                 271 GYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLOSK ---PFTLRWTGYKNSDAGSNGIV 326
                                                                                                                                                                                                                                                                                                                                              327 IVATTRIVT-----DSTIAVTILPFNPSVDKTKII---EILQPIP----TTT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTTTRTNPTDSIDT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYVEYSGNGPKASGGDYCIQS-----SQDMPT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTVTAPPG--GTDSV--IIREPPN-PTVTTTEYWSQSFATTT-----TVTA-PPGGTD 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          535 SVIIREPPNPTVTTTEYWSQSYATTT---VTAPPGGTDSVIIREPPNHTVTTTEYWSQSY 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTAPPGETDTVLIREPPNHTVTTTEYWSQSYATTTTVTAP-PGGTDTVIIREPPNPTVTT 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEYWSQSFATTTTVTAPPGGTDTVIIYESMSSSKISTSSNDITSIIPSFSRPHYVNSTTS 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        825 DLSTFESSSMNTPTSISSDGMLLSSTTLVTESETTTELICSDGKECSRLSSSSGIVTNPD 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       577 ---TSPTSAVTTPTPNA-----TSPTL------GK-----TSPTSAVTTPT 608
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                                                                                                       Ouery Match
Best Local Similarity 22.9%; Pred. NO. 6.1e-11; Indels 378;
Matches 266; Conservative 128; Mismatches 390; Indels 378;
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-783-774-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513
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                                                                1120 EPTDTREQPTTLSTTSKTNSELVATTQATNENGGKSPSTDLTSSLTTGTSASTSANSELV 1179
                                                                                                                                                                                     1180 TSG-SVTGGAVASASNDQSHSTSVTNSNSIVSNTPQTTLSQQVTSSSPSTNTFIASTYDG 1238
                                                                                                                 770 -----PTVTSTGGKANS----TT-----GGKH------TTGHGARTSTEPTTD 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               716 STSSPEP-----RPGTTSQASGPGNSSTSTKPGEVNVTKGTPPQNATSPQAPSGQKTAV 769
                                                                                                                                                                                                                                          803 YGGDSTIPRPRYNATIYLPPSTSSKLRPRWIFTSPPVITAQATVPVPPTSQPRFSNL--- 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 TAGTN-TVTFNDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 TADVNVTINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENATNLFLLELLGAGEL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 SGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQNVPA 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Space, Richard and Jackman, Winthrop, T. TITLE OF INVENTION: Non Splicing Variants of gp350/220 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: IBM PC Comparatible
COMPUTER: STATEM: PC-DOS/MS-DOS
SOCTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04611A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVIR-003/00US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application PC/TUS9504611A GENERAL INFORMATION:
APPLICANT: Spacte, Richard and Jackn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIPICATION:
CLASSIPICATION DATA:
PRIOR APPLICATION NUMBER: 08/229,291
FILING DATE: April 18, 1994
CLASSIFICATION:
ATTORNEY, AGGNT INFORMATION:
NAWE: LUANN CSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFOLLAR
NAME: LUANN CSETT
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR-
TELECOMUNICATION INFORMATION:
TELECHONE: 415-83-5163
TELERA: 380816 COOLEYPA
INFORMATION FOR SEC ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 907 amino acids
TYPE: amino acids
TYPE: .... 11near
                                                                                                                                                                                                                                                                                                       1239 SGSIIQHSTWLYGLITLLSLFI 1260
                                                                                                                                                                                                                                                                                                                                                         860 SMLVLQWAS--LAVLTLLLLV 879
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.005 NTDLTSEPTNTREQPTTLS-TTSNSITED---ITTSQPTGDNGDNTSSTNPVPTVATSTL 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1061 ASASEEDNKSGSHESASTSLKPSMGENSGLTTSTEIEATT-TSPTEAPSPAVSSGTDVTT 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1120 EPTDTREQPTTLSTTSKTNSELVATTQATNENGGKSPSTDLTSSLTTGTSASTSANSELV 1179
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271 GYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSK----PFTLRWTGYKNSDAGSNGIV 326
                                                                    327 IVATTRTVT------DSTTAVTTLPFNPSVDKTKTI---EILQPIP-----TTT 366
                                                                                                  174 VRAQGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPGDNKFNITCS 233
                                                                                                                                        367 ITTSYVGVITSYLIKTAPIGETATVIVDVPYHTTITVTSEWTGTITTTTTTNPIDSIDT 426
                                                                                                                                                                378 NI------SGAFASNRTFDITVSGLGT-----APKTLIITRT----- 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            672 N------PETLSPSTSDNSTSHMPLLTSAHPTG--GENITOVIPA-SISTHHV 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STSSPEP-----RPGTTSQASGPGNSSTSTKPGEVNVTKGTPPQNATSPQAPSGQKTAV 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           770 ------PTVTSTGGKANS----TT-----GGKH------TTGHGARTSTEPTTD 802
                                136 --------FGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTNITAV 173
                                                                                                                                                                                                               WWQVPLPNPTVSTTEYWSQSFATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFAT 486
                                                                                                                                                                                                                                               LYVEYSGNGPKASGGDYCIQS-----SQDMPT 317
                                                                                                                                                                                                                                                                                   487 TTTVTAPPG--GTDSV--IIREPPN-PTVTTTEYWSQSFATTT-----TVTA-PPGGTD 534
                                                                                                                                                                                                                                                                                                                                                          SVIIREPPNPTVTTTEYWSQSYATTT---VTAPPGGTDSVIIREPPNHTVTTTEYWSQSY 592
                                                                                                                                                                                                                                                                                                                                                                                                                                593 ATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFATTTTVTGPPSGTDTVIIREPP-- 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NPTVTTTEYWSQSYATTTT----ITAPPGETDTVLIREPPNHTVTTTEXWSQSYATTT 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           706 VTAPPGETDTVLIREPPNHTVTTTEYWSQSYATTTTVTAP-PGGTDTVIIREPPNPTVTT 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  765 TEYWSQSFATTTTVTAPPGGTDTVIIYESMSSSKISTSSNDITSIIPSFSRPHYVNSTTS 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLSTFESSSMNTPTSISSDGMLLSSTTLVTESETTTELICSDGKECSRLSSSSGIVTNPD 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNESSIVTSTVPTASTMSDSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLSS 944
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51;
Sequence 40, Application US/08616844
Patent No. 549578
CENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
TITLE OF INVENTION: TEATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: New York
CITY: New York
CITY: New York
COUWRRY: USA
COUWRRY: USA
COUWRRY: USA
COUWRRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 -----IATALTSQSGNLASESLHLPSSSSEFDERIAAFQTKSGTASEMGTERAMG 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 SRLQSKPFTLRWTGYKN---SDAGSNGIVIVATT----RTVTDSTTAVTTLPFNPSVDKT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 VIVDVPYHTTTTVTSEWT-----GTITTTTTTRTNPTDSIDTVVVQVPLPNPTVSTT 441
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                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER. IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,844
FILING DATE: 15-MAR-1996
CLASSIFICATION: 800
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/595,53
FILING DATE: 07-UN-1995
RILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATORNEY/AGENT INFORMATION:
NAME: CORREZE, LAARRA
PORTECT AND NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATORNEY/AGENT INFORMATION:
NAME: CORREZE, LAARRA
PORTECT AND NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 30,44
REFERENCE/DOCKET NUMBER: 785:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 869-8864
TELEFAX: (212) 869-8864
TELEX: 6641 PENUR 864
INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: CORUZZI, LAURA A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-616-844-40
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Sequence 40. Application US/08599654
Patent No. 5881232
Patent NO. 5881242
APPLICANT: FALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TEAMBAIT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------TSSTKV----LPP-VVSSNTD--LTSEPTNTREQPTTLSTTSNSITED 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1033 ITTSQPTGDNGDNTSSTNPVPT··VATSTLASASEEDNKSGSHESASTSLKPSMGENSGL 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTSTE---IEATTTSPTEAPSPAVSSGTDVTTEPTDTREQPTTLSTTSKTNSELVATTQA 1147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1148 TNENGGKSPSTDLT-----SSLTTGTSASTSANSELVTSGSVTGGAVASASNDQS 1197
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                                                                                                            TVT--APPGGTDTVIIREPPNHTVTTTEYWSQSFATTTT-VTGP----PSGTDTVIIREP 649
                                                                                                                                                                                                 SDSTVQSGGSHTALGDRSYSESSTSSESLNSSAPRGERSTLEDSREPGQALGDSSANA 548
                                                                                                                                                                                                                                                                                                                                                                                549 EDRTSGVPSLGTHTLATVTGNGERTLRSVTLTNTSMSTTSGEAGSPAAAMPQETEGASLH 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSITDNSSSSD--IVESSTSYIKISNSSH---SEYSSFS---HAQTERSNISSYDGEYAQ 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 PSTESPVLHTSNLPSYTPTINMPNTSVVLDTDABEVSDSSSSSSSSSSSSGPLPLPS 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781 VSQSHHLFSSILPSTRASVHLLKSTSDASTPWSSSPSPLPVSLTTSTSA------PLS 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   833 VSQTTLPQSSSTPVLPRARETPVTSFQTSTMTSFWTMLHSSQTADLKSQSTPHQEKVITE 892
                                                                                                                                                                                                                                                                                                                                              -------PNHTVTTT----EYWSQSYA-TTTTVTAPPGETDTVLIREPPN-----H 724
                                                                                                                                                                                                                                                                                                                                                                                                                                      TVTTTEYWSQSYATTTTVTAPPGGTDTVIIREPPNPTVTTEYWSQSFATT------ 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            609 VNVTDDMGLVSRSLAASSALGVAGISYGQVRGTAIEORTSSDHTDHTYLSSTFTKGERAL 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TVTAPPGGTDTVIIYESMSSSKISTSSNDITSIIPSFSRPHYVNSTTSDLSTFESS--- 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SMNTPTSISSDGMLLSSTTLVTESETTTELICSDGKECSRLSSSGIVTNP 883
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TD-----SVIIREPPNPTVTTTEYW----SQSFATTTTVTAPPGGTDSVIIREPPNPTV
                                                                               547 TTTEYWSQSYATTTTVTAPPGGTDSVIIREP--PNHTVTTTEYW-----SQSYATTT
                                                                                                                                                                                                                                                         650 PNPTVTT----TEYWSQSYATTTTI-----TAPPGETDTVL-IREP-----
                       947 LKTSOPLMTTPGTLSSTASLVTGPIAVOTTAG----KQLSLTHPEI---LVPQISTEGGI
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301 SRLOSKPFTLRWTGYKN---SDAGSNGIVIVATT----RTVTDSTTAVTTLPFNPSVDKT 353 134 STVSSKEGVWVQTSGKSHAASDAPENLTLLAETADARGRSGSSSRTNFTILPVGYSLE-- 191 354 KTIEILQPIPTTTTTTSYVGVTTS-----390 -----IATALTSQSGNLASESLHLPSSSSEFDERIAAFQTKSGTASEMGTERAMG 241 442 EYWSQSFATTTT-----VTAPPGGTDTVIIREPPNHTVTTTEYWSQSFATTTTVTAPPGG 496 287 --WLHFYRTAASSPLLDLSSPSESTEKL-----NNSTGLQSSSVSQTKTMHVATVF 335 882 -----RNSRVTGNPGDEEFI---EPSTENEFGLTSLRWQNDSPTFGEHQLASSS 428 391 VIVDVPYHTTTTVTSEWT-----GTITTTTTTRTNPTDSIDTVVVQVPLPNPTVSTT TD-----SVIIREPPNPTVTTTEYW---SQSFATTTTVTAPPGGTDSVIIREPPNPTV 547 TTTEYWSQSYATTTTVTAPPGGTDSVIIREP--PNHTVTTTEYW-----SQSYATTT 597 TVT--APPGGTDTVIIREPPNHTVTTTEYWSQSFATTTT-VTGP----PSGTDTVIIREP Indels 330; NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PERNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New YORK
COUNTRY: USA
ZIE: 10036-Z711
COMPUTER READABLE FIDOPY disk
COMPUTER: TENDABLE FIDOPY disk
COMPUTER: PEDOPY ASK
COMPUTER: PETCHING SYSTEM
COMPANIES: PETCHIN PRELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA: Query Match 5.0%; Score 322; DB 2; Los Best Local Similarity 21.2%; Pred. No. 1.4e-10; Matches 246; Conservative 159; Mamatches 428, APPLICATION NUMBER: 05/08/599,654
FILING DATE: 09-FEB-1996
FLOASIFICATION: 800
PRIOR APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-041
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 anino acids (212) 869-8864 5141 PENNIE TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-599-654-40 amino acid STRANDEDNESS: TELEFAX: 497 ò g ò qq ŏ 

51;

650 PNPTVTT----TEYWSQSYATTTTI-----TAPPGETDTVL-IREP------- 685 

e Fri Oct 4 08:13:45 2002

686 ------PNHTVTTT----EYWSQSYA-TTTTVTAPPGETDTVLIREPPN-----H 724

ò	833	SMNTPTSISSDGMLLSSTTLVTESETTTELICSDGKECSRLSSSSGIVTNP 883
qc	721	PSTESPVLHTSNLPSYTPTINMPNTSVVLDTDAEFVSDSSSSSSSSSSSSSGPPLPLPS 780
Ì	884	DSNESSIVTSTVPTASTMSDSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLS 943
qq	781	VSQSHHLFSSILPSTRASVHLLKSTSDASTPWSSSPSPLPVSLTTSTSAPLS 832
ογ	944	SSVTSLTQLSSIPSVSES-ESKVTFTSNGDNQSGTHDSQSTSTEIEIVT- 991
qq	833	VSQTTLPQSSSTPVLPRARETPVTSFQTSTMTSFWTMLHSSQTADLKSQSTPHQEKVITE 892
ογ	992	TSSTKVLPP-VVSSNTDLTSEPTNTREQPTTLSTTSNSITED 1032
qq	893	SKSPSLVSLPTESTKAVTTNSPLPPSLTESSTEGTLPATSTNLAQMSPTFTTT 946
ò	1033	
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0y	1091	TTSTEIEATTTSPTEAPSPAVSSGTDVTTEPTDTREOPTTLSTTSKTNSELVATTQA 1147
QQ	1000	STERNRVIVDATTGLIPLTSVPTSAKEMITKLGVIAEYSP 1039
ογ	1148	
QQ	1040	SERSECTSPSPQTTVVSTAEDLAPKSATFAVQSSTQSPTTLSSSASVNSCAV 1091
ò	1198	HSTSVTNSNSIVSNTPQTTLSQQVTSSSPSINTFIASTYDGSGS 1241
qq	1092	- NPCLHNGECVADNTSRGYHCRCPPSWQGDDCSVDVNECLSNPCPSTATCNNTQGS 1146
À	1242	IIQHSTWLYGLITLLSLFI 1260
g G	1147	FICKCPVGYOLEKGICNLVRTFV 1169

Search completed: October 3, 2002, 15:32:32 Job time: 359 sec

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October 3, 2002, 15:29:03; Search time 29.15 Seconds (without alignments) 4153.433 Million cell updates/sec
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6495
1 MLQQPTLLFLYLSIASAKTI.....SIIQHSTWLYGLITLLSLFI 1260
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                          Scoring table:
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stal number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

earched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

240 240

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181 181 361 361 421

TDSIDTVVVQVPLPNPTVSTTEYWSOSFATTTVTAPPPGGTDTVIIREPPNHTVTTEYW 480

	membrane glycoprot	gastric mucin (cto hypothetical prote	nypornetical 129.5 a-aqqlutinin core	MSB2 protein - yea	hypothetical prote	probable membrane	host cell vsac [	mucin 3 - human (f	hypothetical prote	ENTS		albicans)	C;Species: Candida albicans C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000		A.R.; Livi, G.P.	lated to a Saccharomyces cerevisiae sexual				A;Cross-references: EMBL:L25902; NID:g704426; PIDN:AAC41649.1; PID:g704427 C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosida	495; DB 2; Length 1260;	.7e-273;	Mismatches 0; Indels 0; Gaps 0;
T21389 A83412	T45462 T45463	2521	T40//8 A41258	525370	T22696	5862	7,50	PC4395	1678	ALIGNMENTS		(Candida a	ton 13-			ains re	766717			D: 97044	Score 6495;	Pred. N	
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	000											ast	r r	1	Sha 995	51:	101			902	100.08;	100.08;	φ
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443.5	430.5	423.5	4.18.5	415.5	412	409.5	40400	401.5	400.5		1	iin-like	s: Cand 27-Apr-	1on: S6	L.L.; robiol.	Candid	ion: S6	: preli	es: 1-1	referen	Match	Best Local Similarity	Matches 1260;
30	01 EN 60	3 C C	35 37	38	40	41	4 4	44	45		RESULT	S60896 agglutinin-like protein	C;Species: Candida albicans C;Date: 27-Apr-1996 #sequen	C, Accession: \$60896	R; Hoyer, L.L.; Scherer, S.; Shatzman, Mol. Microbiol. 15, 39-54, 1995	A; Title: Candida albicans ALSI: domains related	A; Accession: S60896	A; Status: preliminary A: Molecule type: DNA	A; Residues: 1-1260 <hoy></hoy>	A; Cross- C; Superf	Ouery Match	Best	Matche

29;

	Query Match 49.2%; Score 3194; DB 2; Length 1419; Best Local Similarity 49.5%; Pred. No. 9.8e-131; Matches 708; Conservative 182; Mismatches 355; Indels 186;	Qy 1 MLQOFTLLFLYLSIASAKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGT:	Qy 61 ANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEBFTTFSTLTCTVNDALKS	Qy 121 SIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDP	Oy 181 SAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTWGFSSSNGDVAIDCSNIHIGITKGLND	Qy 241 WNYPVSSESFSTRTCTSNGIQIKYONVPAGYRPFIDAYISATDVNQYTLAYNDYTCAG   : : :	Oy 301 SRLOSKPETLRWIGYKNSDAGSNGIVIVATTRTYTDSTTAVTTLPENDSVDKTKTIETLO	Qy 361 PIPTTITTSYGYTTSYLAKTAPIGETATVIVOVPHTTTTVTSEWIGTITTTRTNP	Qy 421 TDSIDTYVVQVPENPTVSTTEYWSGSFATTTTVTAPPGGTDTVIIREPPNHTVTTTEYW	Qy 481 SOSFATTTTVTAPPGGTDSVIIREPPNPTVTTTEVMSOSFATTTTVTAPPGGTDSVIIRE	Qy 541 PPNPTVTTEYWSQSYATTTTVTAPPGGTDSVIIREPPNHTVTTEYWSQSYATTTTVTA 	Qy 601. PPGGTDTVIIREPPNHTVTTEYWSQSFATTTTVTGPPSGTDTVIIREPPNPTVTT	Qy 658EYMSQSYATTTITAPPGETDTVLIREPPNHTVT	Oy 692  Db 721 SSSSIESSTLSSS  Qy 726 VTTEYWSGSYAT	ABB8883.1  QY 857 ETTTELICSDGKECSRLSSGIUTN-PDSNESSIVETNPASTMSDSLSSTDG-I
Db 421 TDSIDTVVVQVPLPNPTVSTTEYWSQSFATTTTVTAPPGGTDTVIIREPPNHTVTTTEYW 480	Oy 481 SQSFATTTVTAPPGGTDSVIIREPPNPTVTTEVWSQSPATTTVTAPPGGTDSVIIRE 540	Oy 541 PPNPTVTTEXWSOSYATTTVTAPPGGTDSVIIREPPNHTVTTEXWSOSYATTTVTA 600   111111111111111111111111111111111	Qy 601 PPGGTDTVIIREPPNHTVTTTEYWSQSFATTTTVTGPPSGTDTVIIREPPNPTVTTTEYW 660	QY 661 SOSYATTTITAPPGETDTVLIREPPNHTVTTEYWSQSYATTTTVTAPPGETDTVLIRE 720	OY 721 PPNHTVTTTEYMSOSYATTTTVTAPPGGTDTVIIREPPNPTVTTTEYMSOSFATTTTVTA 780	781 PPGGTDTVIIXESMSSSKISTSSNDITSIIPSFSRPHVVNSTTSDLSTFESSSMNTPTSI 840	Qy 841 SSDGMLLSSTTLVTESETTTELICSDGKECSRLSSSSGIVTNEDSNESSIVTSTVPTAST 900	OY 901 MSDSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSE 960	OY 961 SESKYTFTSNGBNQSGTHDSQSTSTELEIVTTSSTKVLPPVVSSNTDLTSEPTNTREQPT 1020	QY 1021 TLSTTSNSITEDITTSQPTGDNGDNTSSTNPVPTVATSTLASASEEDNKSGSHESASTSL 1080	OY 1081 KPSWGENSGLTTSTEIEATTTSPTEAPSPAVSSGTDVTTEPTDTREQPTTLSTTSKTNSE 1140	OY 1141 LVATTOATNENGCKSPSTDLTSSLTTGTSASTSANSELVTSGSVTGGAVASASNDOSHST 1200	1201 SVTNSNSIVSNTPOTTLSQQVTSSSPSTNTFIASTYDGSGSIIQHSFWLYGLITLLSLFI 1260	RESULT 2 T30531 agglutinin-like adhesin - yeast (Candida albicans) C.Species: Candida albicans C.Species: Candida albicans C.Species: Candida albicans C.Accession: T30531 R.Gaur. N.K.; Klotz. Infect. Immun. 65, 5289-5594, 1997 A.Title: Expression, cloning, and characterization of a Candida albicans gene, A:Reference number: 220847; MUID:98053977 A.Status: preliminary: translated from GB/EMBL/DDBJ A.Status: preliminary: translated from GB/EMBL/DDBJ A.Molecule type: DNA	PID:92522219; PIDN:A

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Oy 287OYTLAYTNDYTCAGSRLQSKPFILRWTGYKNSDAGSNGIVIVATT 331  259 SQPNCTIPDDSNYTVSTITTTEPWTGTFISTSTEMTTVTGTNGVPTDETVILTT 314  Qy 332 RTVTDSTTAYTLPFNPSVDKTKT	416 TRINPIDSIDIVAVOUPLENPT-VSTTEYWSOSEATTTTVTAPPG-GTDTYU	Oy 562 VTAPPG-GTDSVIIREPPNHTVTTTEYMSOSYATTTTVTAPPG-GTDTVI 609	Qy         659 YWSQSYATTTTITAPPGETDIVLIREPPNHTVTTTEYWSQSYATTTT 705           III	Qy         754 IREPPRPTVTTTEYWSQSFATTTTYVAPPGGTDTVIIYESMSSSKISTS 802           b         11   1   1   1   1   1   1   1   1   1	Qy 857 ETTTELLCSDGKECSRLSSSGIVTNPDSNESSIVTSTVPTASTWSDSLSSTDGISATSS 916 :::	OY 977 THDSOSTSTEIEIVTISSTKVLPPVVSSNTDLTSEPTNTREOPTILSTTSNSITED1 1033  1062SEQTTLVTVTSCESHVCTESISSAIVSTATTWCSGATTETTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
Qy         912 SATSSDNVSKSGVSVTTETSVTTIOTTPNPLSSSVTSLTQLSSIPSVSESESKVTFTS 969           bb         1014 SITDNPNIDSCSTASASSTKSSVSVSVTVNSILLSETS-TLSSDBXTS-SDTSISSTT 1070           Qy         970 NGDNQSGTHDSQSTSFIEIVTS-STKVLPPVVSSNTDLTSEPTNTR 1016           Db         1071 NSDTGNINAGSSHTSTASIKESSIQKTGVTLSSSYLSTKLSSTSDITIELITTELITTEL 1130           Qy         1017EQPTTLSTTSNSITEDITTSQPTGDNGDNTSSTNPVPTVATSTLA 1061           Db         1131 TYTEDREPNPTTRSPSSHSFTSSNNKVLSKONDESSTNETSCHAPPTNYTTNSSTLANDED	1062 SASEEDNESSHERSASSISTERSELTTSPTEAPSPANSSGTD    1	Db 1309 PSKTKSIEESIMNPDSTNETNNGFIATLSQAQVPSSSIHSELLSTTTAKTTDASMNGDSA 1368  Qy 1209 VSNTPQTTLSQQVTSSSPSTNTFIASTYDGSGSIIQHSTWLYGLITLLSLE 1259	hypothetical protein YALO63c - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 22-Oct-1999 C;Accession: S51959 R;Bussey, H:, Kaback, D.B.; Zhong, W.Y., Vo, D.T.; Clark, M.W.; Fortin, N.; Hall, J.; Ouel submitted to the EMBL Data Library, August 1994 A;Description: The sequence of chromosome 1 of Saccharomyces cerevisiae.	A; Accession: S21959 A; Accession: S21959 A; Mocedule type: DNA A; Mesidues: 1-1367 < 48US> A; Cross-references: EMBL:U12980; GSPDB:GN00001; MIPS:YAL063c C; Genetics: A; Gene: MIPS:YAL063c A; Map position: 1L	Ouery Match  Best Local Similarity 28.1%; Pred. No. 2.9e-33; Matches 410; Conservative 214; Mismatches 469; Indels 364; Gaps 84;  Oy 28 NSLTWSNAANYAFKGGYPTWNAVLGWSLDGTSANPGDFFTLAMPCVFKYTTSOTS 83	4

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84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 FYTTPTNV-TLEMTGYFLPPQTGSYTFKFATVDDSAILSVGGATAFNCCAQQQPPITSTN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 LTADGVK-----YATCQFYSGEEFTTFSTLTCTVNDALKSSIKAFGT----VTLP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 IAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTV-DPSAYLYASRVM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 PSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESF 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 TITEPWIGTETSTSTEMTTVIGINGVPIDETVIVIRTPITASTIITTTEPWNSTFTSTST 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYTKICTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 -----IEILOPIPTTTTT-----SYVGVTTSYLTKTA----PIGETATVIVDVPYH 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 PTDETIIVIRTPTTATTAMTTTQPWNDTFTSTSTELTTVTGTNGLPTDET-IIVIRTPTT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 WSQSFATT----TTVTAPPG-GTD--TVIIREPPNHT--VTTTEYWSQSFATT----TTV 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  539 REPPNPT--VTTTEYWSQSYATT----TTVTAPPG-GTDS--VIIREPPNHT--VTTTEY 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        588 WSQSYATT----TTVTAPPG-GTD--TVIIREPPNHTV--TTTEYWSQSFATT----TTV 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               635 T---GPPSGTDTVIIREPPNP--TVTTTEYWSQSYATT----TTITAP---PGETDTVLI 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         683 REPPNHTV--TTTEYWSQSYATT----TTVTAPPGE-TD--TVLIREPPNHTV--TTTEY 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       732 WSQSYATTTTVTAPPGGTD-----TVIIREPPNPTV--TTTEYWSQSFATTTTVTAPP 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         913 WIGTFISTSTEMTHVIGINGVPIDETVIVIRIPISEGLISTITEPWIGTFISTSTEVITI 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGT-----DTVIIYESMSSSKI------816
                                                                                                                                                                             59 TSANPGDIFTLNM-----TSCVFKYTTSQ------TSVD 85
                                                                                                                                  2 LOOFTLLFLYLSIASAKT-----ITGVFDSF-----NSLTWSNAANYAF----- 40
                                                                                                                                                                                                                                                                    239 ----DGTTVSDDFEG-----YVXSFDD-----DLSQSNCTVPDPSNYA-VSTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 RWTGYKNSDAGSNGI---VIVATTRTVTDSTTAVTTL-PFNPSVDKTKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAPPG-GTDS--VIIREPPNPT--VTTTEYWSQSFATT----TTVTAPPG-GTDS--VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 ELTIVIGINGVRIDETII-----VIRIPTIATITITIEPWNSTFISTEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 TTT--TVTSEWIGTIT-----TTTTRIN--PIDSIDTVVVQVPLPNPTVSTT----EY
Query Match 14.5%; Score 939; DB 2; Length 1537; Best Local Similarity 25.6%; Pred. No. 3.3e-33; Matches 414; Conservative 246; Mismatches 520; Indels 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Association type: DNA
Residues: 1.1537 < Cass.
Rivatari, J.: Takata, Y.: Ogawa, M.: Sahara, H.; Roshino, S.; Onnela, M.L.; Alraksinen, Yeast I), 211-225, 1994
A;Title: Molecular cloning and analysis of the yeast flocculation gene FLOI.
A;Reference number: S43543; MUID:94262325
A;Recession: S43543; MUID:94262325
A;Rocession: S43543; MUID:9426432; M., 520-549, T., 551-608, L., 610-636, M., 638-69
A;Cross references: EMBL:X78160
B;Miller: S438, M., 430-463, T., 465-473, M., 475-518, M., 520-549, T., 551-608, L., 610-63
A;Recession: S57851
A;Recession: S
                                                                                                                                                                                                                                                                                                                               flocculation protein FLOI precursor - yeast (Saccharomyces cerevisiae)

%Alternate names: protein YAR050w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 29-Oct-1999
C;Accession: S53465; S43543; S57851; S31230; S57349
R;Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kabac submitted to the EMBL Data Library, February 1994
A;Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Molecule types: DNA A.Molecule types: 1-296,927-1516, TAYWPVVV < TEU> R.Bidard, F.: Bony, M.; Blondin, B.; Dequin, S.; Barre, P. Tenst 11, 809-822, 1995 A.Thile: PNE Saccharomyces cerevisiae FLOI flocculation gene encodes for a cell surface reference number: S57349; MUID:96090130
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C; Keywords: duplication; glycoprotein; transmembrane protein
C; Keywords: duplication; glycoprotein; transmembrane protein
C; Keywords: duplication; glycoprotein; transmembrane protein
E; 124. Domain: stepata A2 - RAA2-
F; 125-1537, Product: flocculation protein FLOI #status predicted <MAT>
F; 125-1276, Domain: repeat A3 - RAA3-
F; 1043-1081, Domain: repeat B1 - RB12-
F; 125-1276, Domain: repeat B2 (partial) #status atypical <RB2>
F; 125-1377, Domain: repeat B2 (partial) #status atypical <RB2>
F; 125-1347, Domain: repeat B3 - RB13-
F; 135-1347, Domain: repeat B4 - RB4>
F; 1408-1416, Domain: repeat B4 - RB4>
F; 1408-1416, Domain: repeat B3 - RB13-
F; 141-1425, Domain: repeat C3 - RC2>
F; 1426-1434, Domain: repeat C3 - RC3>
F; 135, 187, 262, 1114, Mainding site: carbohydrate (Asn) (covalent) #status predicted
1290 VIGHSSSVVSVSETGNTKSLTSSGLSTMSQQPRSTPASSMVGSSTASLEISTYAGSANSL 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
Residues: 1243-1274;1308-1339;1359-1390 <BID>
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A;Cross-references: SGD:S0000084; MIPS:YAR050w
                                                                                                  1244 QHSTWLYGLITLLSLFI 1260
                                                                                                                                                                 1350 LAGSGLSVFIASLLLAI 1366
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Accession: S53465
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SLKPSMGENSGLTTS--TEIEATTTSPTEAPSPAV------SSGTD---- 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---TTSSTKVLPPVVSSNTDLTSEPTN-----TREQPTTLST--TSNSITEDITTSQP 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1049 STKPG-GE---ITTTFVTKNIPTTYLTTIAPTPSVTFVTNFTPTTITTVCSTGTNSAGE 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      870 SSSSNITSSAPSSIPFSSTTESFSTGTTVTPSSSKYPGSQTETSVSSTTETTIVPTKTTT 929
                                                                         221 GDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYI 280
                                                                                                                                                                                                                                                                                                          206 GGTKSSTTTSSTSESSTTTSSTSESSTTT----SSTSESS----TTTSSTSESSTSS 254
                                                                                                                                                                                                                                                                                                                                                                                       341 VITLPENPSVDKTKTIEILQPIPTTITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTVTSEWTGTITTTTTTTTT---PTDSIDTV-VVQVPLPNPTVSTTEYWSQ--SFATTTTV 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 TPCTKKKTTTSKTCTKKTTTPVPTPSSSTTESSSAPVPTPSSSTTESSSAPVTSSTTESS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSYATTTT-VTAPPGGTD 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     571 SVIIREPPNHTVT--TTEYWS-----QSYATTTTVTAPPGGTDTVIIREP-PNHTVTTTE 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       623 YWS-----QSFATTTTVTGPPSGTDTVIIREP-PNPTVTTTEYWSQSYATTTTITAPPGE 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          677 IDTVLIREPPNHTVTTTEYWSQSYAT --- TTTVTAPPGETDTVLIREPPNHTVT -- TTE 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576 SSSAPV---PTPSSSTTESSSAPVPTPSSSTTESSSAPAPTPSSSTTESSSAPVTSSTTE 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 731 YWS-----QSYATTTTVTAP---PGGTDTVIIREP-PNPTVTTTEYWSQSFATTTTVTAP 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  633 SSSAPVPTPSSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTE--SSAPVTSSTTES 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSAPVTSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTESSSA 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      930 SVITPSITITITIVCSIGINSAGETISGCSPKIVITIVPTITITISVITISITITITVCS 989
                                                                                                                                                                                                                                281 SATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 STTAPATPT----TTSCTKEKPTPPTTTS------CTKEKP-----TPPHHDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455 TAP---PGGTDTVIIREPPNHTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVT
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                                                                                                                                                  178 G----CNNYD---NQGHSQTDFP----GFYWNIDCDNN----
140 SCQVWMPNFQIQFE---
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Accession: A26877
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Accession: B2781
Accession: B2612
Accession: B2781
                                                                                                                                    Judan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
Nicterate names: extracellular glucoamylase; mucin-like protein MUCI; protein YIR019c (Species: Saccharomyces cerevisiae)
Cispecies: Saccharomyces cerevisian 10-Sep-1999 #text_change 12-Nov-1999
Cispecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
Right of the EMBL Data Library, October 1994
Alrecasion: $48478
Alrecasion: $4847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: nucleic acid sequence not shown
Molecule type: DNA
Residues: 1-1367 <LAM>
CLOSS-references: GB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387
Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --NIDLKYLWSLKIIGVTGPKGTVQLYGYNENTYLIDNPTDFTA----TFEVYATQDVN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 353; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 TVNDALKS--SIKAFGTVTLPIAFNVGGTGSSTDLEDSKC-FTAGTNTVTFN-DGDKDI- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MORPFLLAYLVLSLL------FNSAL------GFPTALVPRG-SSEGTS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLQQFTLLFLYLSIASAKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNSIVNGCPNLDFNWHMDQQNIMQYTLDVTSVSWVQDNT-YQITIHVKGKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: SGD:MUC1; STA2; MAL5; DEX2; SGD:S0001458
Cross-references: MIPS:YIR019c; SGD:S0001458
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A:Map position: X
A:Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 20
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A;Experimental source: strain Bristol N2; clone K06A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein K06A9.la - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Accession: T44434
R.Geisel, C.: Gattung, S.
Rydeisel, C.: Gattung, S.
Rydeisel, C.: Gattung, S.
Rymbalted to the RMID Data Library, December 1996
A.Description: The sequence of C. elegans cosmid K06A9.
A.Reference number: 221525
A.A.Accession: T34434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1076 GSTVSTVSG--STGSTITGESTVSGSTESTVTAESTVSGSSVSTVSGNT--GSTITGE-S 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SESKVTFTSNGDNQSGTHDSQSTSTEIEIVTTSSTKVLPPVVSSNTDLT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1068 NKSGSHESASTSLKPSMGEN--SGLTTSTEIEATTTSPTEAPSPAVSSGTDVTTEPTDTR 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1126 EQPTTLSTTSKTNSELVATTQATNENGGKSPSTDLTSSLTTGTSASTSANSELVTSGSVT 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1186 GGAVASASNDQSHSTSVTNSNSIVSNTPQT-TLSQQVTSSSPST---NTFIASTYDGSGS 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .010 SEPTNTREOPTILSTISNSITEDITTSOPTGD--NGDNTSSTNPVPTVATSTLASASEED 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLSSTDGISATSSDNVSKSGVSV--TTETSVTTIQTTPNPLSSSVTSLTQLSSIPSVSE- 960
  ---TTTEY 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         660 WSQSYATTTTTAPPGETDTVLIREPPNHTVTT-TEYWSQSYATTTTVTAPPGETDTVLI
                                                                                                                                                                             719 REPPN-----HTVTTTEYWSQSY------ATTTTVTAPPGGTDTVIREPPN
                                                                                                                                                                                                                                                                                                         629 STISGS---SASTVTGSTVTEASTISGSTESSTIPGSTESTVSEASTVSGSSVSTVSGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIPGSTES-----TITGSTVTGESTVSGSTGSTITEGSTISESTMTTVGVSTGSTITGES
                                        454 PLPSQSTSLSMSSLSTYTPSSSTAGATSPATQQSTKPTIGTSMSSGPTTVAPGASTESTV
                                                                                                                               514 LQSSTPSGTTVTLPSGSSTATAGTSPQASTVTTVTDISTVSGSTVTSQTA-----ESSLS
                                                                                                                                                                                                           760 PTVTTTEYWSQSFATTTTVTAP------PGGTD-TVIIYESMSSSKISTSSNDI
                                                                                                                                                                                                                                                                                                                                                                807 TSIIPSFSR-PHYVNSTTSDLSTFESS--SMNTPTSI------SSDGML
                                                                                                                                                                                                                                                                                                                                                                                                        686 ESTSAGASTVSGSTGSTVSDSSTISDSTGSTNAPGSTESTVTGSSVSTVSGSTGPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSSTTLVTESETTTELICSDGKECSRLSSSSGIVTNPDSNESS----IVTSTVPTASTMSD
-----YWSQSFATTTVTGPPSGTDTVIIREPPNPTV----
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A;Molecule type: DNA
Residues: 1-232 <GEI>
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A;Gene: CESP:K06A9.1a
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A;Introns: 42/1; 78/3; 106/3; 135/2; 161/2; 224/1
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
                                                                                                                                                                                                                                                                                                                                                     hypothetical protein H02P09.3 - Caenorhabditis elegans
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Gelsei, C.; Harmon, G.
Jubmitted to the EMBL Data Library, July 1998
Abescription: The sequence of C. elegans cosmid H02F09.
A; Reference number: 221330
A; Accession: T3336
A; Accession: T3336
A; Accession: T3336
A; Accession: T3356
A; Cross-references: EMBL; AF077538; PIDN: AACG4622.1; GSPDB: GN00028; CESP: H02F09.3
A; Experimental source: strain Bristol N2; clone H02F09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                           SSLTTGTSASTSANSELVTSG-----SVTGGAVASASNDQSHSTSVTNSNSIVSN---- 1211
                                                                                                         1212 ------TPQTT---LSQQVTSSSPSTN------TFIASTYDGSGSIIQ 1244
                                                                                                                                    213 TMGFSSSNG------DVAIDCS-----NIHIGITKGLNDWNYPVSSESFSYTKT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 TVSLCNSNSEPQISSLRFKRDANTDCSFNANKNQLRNFLTSSAEDANFILTTYSGTSTKT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------CTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 EPLTKQLALDQLEAIKADGSSAVKQSSAIESYDP--SAY-SNTDLVFFTPCQTN----- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 SRLQSKPFTLRWTG----YKNSDAGSNGI-----VIVATTRTVTDSTT----AVTTLPFN 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSVDKTKTIEILQPIPTT---TITTSYVGVTTSYLTKTAP----IGETATVIVDVPYHT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTEDISNKINNILNIGTTQTPPVTTSTMATTTANVTSAAPNTTVTISTSPTTVVTVP--- 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTVTSEWTGTITTTTTTTTDSIDTVVVQVPLPNPTVSTTEYWSQSFATTTTVTAPPG 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 --STVV-----TVPSTAVTKPSTVVTAPSTVVTVP-----STVVTKPNTVVTSSPTVA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 TTEYWSQSFATTTVTAPPGGTDSVIIREPPN-PTVTTTEYWSQSYATTTVTAPPGGTD 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVIIREPPNHIVITIEYWSQSYAIITTVTAPPGGIDIVIIREPPNHIVITIE------ 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 -----YDGIEDDIKNVQTAINKVITKTFVIVSLSLNSTDMNSRYGEAAHNIPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 1275; Ba 2; Length 1275; Bast Local Similarity 26.8%; Pred. No. 8:66-21; Matches 376; Conservative 151; Mismatches 449; Indels 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: H02F09.3
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1284 YET 1286
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Ma	Query Match 10.0%; Score 646.5; DB 2; Length 2232; Best Local Similarity 23.5%; Pred. No. 2.3e-20; Matches 361; Conservative 227; Mismatches 543; Indels 405; Gaps	62;	
οy	12 LSIASA		
g	Db 274 LSSSTIQSS&GTFPSSVASSPSTVGSTSGAASSSSYATVSTIAGSTGFTTPVPGSSSTI 33	3	
ογ	Qy 70 NMPCVEKYTISQTSVDLTADGVKYATCOFYSGEEFTFSTLTCTVNDALKSIKA 12.	4	
qq	Db 334 GSSTPSASSSSSGTMSTISGSTGSTVTVVPGSSSTFASSTPIASSSSP 381		
ογ	125	e	
g	Db 382 GSTVTVAPGSSSTYGSSTPSASSSSSGTMSTNSGSTGSTVTVAPVSSSTF 431	1	
ŏ	OY 184 LYASRVMPSLNKVTTLEVAPQCENGYTSGTMGFSSSSNGDVAIDCSNIHIGITKGLNDWNY 24:	e	
	432 GSSTPIASSSSSSTVTVVSGSSSTYGSSTPSASSSSAGTASTISGSTGSTATIV 486		
ŝ	UY 244 PVSSESF-SYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSR 302	7	
QQ	Db 487 PGSSSSVGSSTQSASPSSPGTMSTVSGPTGSTVTVVPGSSTSPAPSS 533	3	
ò	303	7	
Q	534 SPNPSSSPASTGSTITISGSSSIIVSTVSGSTVSGSTGTSQSTLAS	E	
ò	Qy 348 PSVDKTKTIEILQPIPTTTTTSYNGVTSKLTATAP 384	4	
q	Db 594 SSPQPSSQSPAPNTGSTTPSQTSSQSPSPSMNPSSSTPTGSSQSTITPEGSTASSP 649	6	
ογ	385		
qq	650	,	
ò	Qy 428VVQVPLPNPTVSTTEY#SQ-SFATTTTVTAP 457	7	
QQ	705 PSSTQSSGA	4	
ογ	Qy 458	9	
q	Db 765 ISPAASTISGEMISQGSTQTPGSSVSISAAILISTQQSVSINSPGSIVIRPSIVSGSISS 824	4	
ò	Qy 487 TTTVTAPPGGTDSVIIREPPNPTVTTTEYMSQSFATTTV 526	9	
	825 GSTVTVGSTEASTSGSSVASSSPAPSTSQNPNPSTSSGSSMITQSPYPSQSTSPVESS 882		
	527 TAPPGGTDSVIIREPPNPTVTTEYWSQSVATTTTVTAPPGGTDSVIIREPPNHTVTTTE 586	9	
QQ	883 TTPSPGSPGTTLTSTSPSPSQ	4	
οy	Qy 587 YWSQSYATTTVTAPPGGTDTVIIREPPNHTVTTFEYWSQSFATTTTVTGPPSGT 641	п.	
QQ	Db 925 MTSQGSTQTPGSTGSTVTQPSTVSDSTSSGSTVTVGSTEGSSSPIPSTSQNTNPSTSS 982	2	
δ	642	0	
ΩD	Db 983 GSSMSTQTPQSSQSTSPVESSTSGATSS-SGSPGTTLTSISPSPSSSTIGSSQGS 1037	37	
ογ	Qy 701 ATTTVTAPPGETDTVLIREPNHTVTTTEYWSQSYATTTTVTAPPGGTD 750	0	
Q	Db 1038 TSPVVSTISQGSTETPGSTGSTVTKPSTVSGSASSGSTATMGSTEASSTSGGSS 109	91	
οy	Qy 751 TVIIREPPNPTVTTTEYMSQSFATTTTTVTAPPGGTDTVIIYESMSSKISTSS 803	£	
qq	Db 1092 TSPNPSQSTSPSTSGATSSPGSSGTTLTSISPSPSQSSTIGSSQGSTSPVVSTTS 114	46	
ò	804	·	
요 6 47	Db 1147 GDMTS-QGSTQIPGSTGSTVTQPST-GSGSTSTSGEITSQGSTQTPRSSLSTSPAI 1200	00	

e .

ō	y 864	CSDGKECSRLSSSSGIVTNPDSNESSIVT-STVPTASTMSDSLSSTDGISA 91	13
qq	b 1201	STSTQQSVSTNSPGSTVTQPSTVRGSTSSGSTVTTGSTEGSSTSGSSATSLSSSSPVPS 1	260
Οy		TS-SDNVSKSGVSVTTETSVTT1QTTPNPLSSSVTSLTQLSSIP 9:	56
qq	b 1261	-	317
οy	у 957		93
QQ	b 1318	GSNSSGSTVTIGSSEASTSGSSFKTSPSSISPVPTSSPIPSTTFASSTSGSTISDVSSVS 1	377
οy	у 994		1024
qa	b 1378	TTSLAPLSSSLPSTVPSSTQSFSSTSEGSSKASSSPVPSQTSSTPTNPTGSTESSTLLSS	1437
δ	y 1025	TSNSITEDITTSQPTGDNGDNTSSTNPVPTVATSTLASASEEDNKSGSHESASTSLKPSM	1084
QQ	b 1438	TISGSTOHTTMSKASSCSTSPSTNS-QTGSTVTMGSSSTSGVSTSSASSTQPQM	1490
Qy	y 1085	GENSGLTTSTEIEATTTSPTEAPSPAVSSGTDVTTEPTDTREOPTTLSTTSKTNSE	1140
qq	b 1491	1	550
Qy	y 1141		1184
qa	b 1551	VIMGSSSTSGVSTSASSTQPQMSTSQGSSAGSTVASSTAGLVSTSTVPSSTGIMGST	1608
Οy	у 1185	TGGAVASASNDQSHSTSVTNSNSIVSNTPQTTLSQ1	219
qa	b 1609	SSGTVGSTISESSTIASASSQTGSTVTMGSSSTSGVSTSSASSTQPQMSTSQGSSAGSTV	1668
Qy	y 1220		
qα	b 1669	ASSTTGLVSTSTVPSSTGTMGSTSSGTVGSTISESS 1704	
R	ESULT		
ΞĔÜ	ypotheti	hypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315)	315)
000	Date: 1	<pre>J-May-rate</pre>	001
i ez E	Kuroda,	M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.	.; Cul, L.; O
	C.; Shib	T.; Hattori, N.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. 7 1995-1940	
í	Title:	Whole genome sequencing of meticillin-resistant Stapylococcus and secure of the sequencing of meticillin-resistant Stapylococcus and the sequencing of meticillin-resistant Stapylococcus and the sequencing of meticillin-resistant Stapylococcus and the sequence of the seq	ureus.
ΥĄ	; Accession	Je Humber: A69/36; MOID: 41311334; PMID: 11416140 on: F90073	
A A	Status:	preliminary type: DNA	
Α,	Residue	1 12271 KKUR>	04100
ΑA	; Cross -r. ; Experim	elerences: GB:BAUUUU18; PID:gl3/U2612; PIDN:BAB43/32.1; GSPDB:G ental source: strain N315	NOOT 49
บ่ ๙ั	Genetic;	5 : 1/2/4/7	
	Best Low Matches	Sect 7 accord Similarity 2.3%; Scott 03.7.; De 2.1 Best Local Similarity 2.3%; Pred. No. 5.96-20; Matches 330; Conservative 280; Mismatches 521; Indels 347; Gapa	s 52;
Οy	y 17	ANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFK 7	9
qq	b 297	AITLGTRIDSNKSFHFSGKVNLGNKYEGHGNGGDGIGFAFSPG33	68
٥y	77 Y		28
qq	b 340	-VLGETGINGAAVGIGGLSNAFGFKLDTYHN-TSKPNSAKANADPSNVAGGGAFGAF 39	95
οy	у 129		98

g	396	::     : :   :  VTIDSYGVATTYTSSSTADNAAKLNVQPTNN-TFQDFDINYNGDT 439	qα	1402
οy	187	SRVMPS	δλ	1056
qq	440		qa	1462
ò	237	VONVOTE STREET S	οy	1104
; a	488		qa	1522
į	000	TO A TO THE TABLE	0y	1155
3 8	533	I THE TOTAL CONSONINGS  I THE CONTRACTOR OF THE TOTAL	qu	1582
3	2 2	MATUTAL AMBRICATION OF THE CONTRACTOR OF THE ACTUAL OF THE CONTRACTOR OF THE CONTRAC	0y	1209
5 8	593	NOTATION OF THE PROPERTY OF TH	qq	1642
4	365		RESULT	11. 1(
g	653		T45	T45025 Mucin MUC
ò	393		ΣΩ: () () ()	C; Species: C; Date: 21
qq	710	DSTNNTISCIPINIGTSTISIVSTDASGNKTTTTFKYEVTRNSMSDSVSTSGSTQQSQ 767	R; P	sseyn,
ò	437	TVSTTEYWSQSFATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFATTT 488	A;T	3101. [t]e: F
qq	768	SUSTEMBORGSASTSTSGSIVVSTSASTSKSTSVSLSDSVSASKSLSTSESNSVSSSTST 827	A; Re	sterenc
ογ	489	TVTAPPGGTDSVIIREPPNPTVTTTEYWSQSPATTTTVTAPPGGTDSVIIRE 540	A; Si	catus: olecule
qq	828	SLVNSQSVSSSWSGSVSKSTSLSDSLSNSNSTEKSESLSTSTSDSLRTSTSLSDSL 883	A A	esidues ross-re
ολ	541		8,50 8,00 8,00 8,00 8,00 8,00 8,00 8,00	A; Experime C; Genetics A; Gene: MI
Q	884	SMSTSGSLSKSQSLSTSISGSSSTSASLSDSTSNAISTSTSLSESASTSDSISI 937		
ò	599	TAPPGGTDTVIIREPPNHTVTTEYWSQSFATTTTVTGPSGTDTVII 646	ÕÃ	Query Ma Best Loc
g	938	SNSIANSQSASTSKSDSQSTSISLSTSDSKSMSTSESLSDSTSTSGSVSGSLSIAASQSV 997	×	atches
ò	647		٥y	9
g	866	STSTSDSMSTSEIVSDSISTSGSLSASDSKSMSVSSSMSTSQSGSTSESLSDSQSTSDSD 1057	ΩĐ	2329
è	704	TTVTAPPGETDTVLIRE	οy	119
Q	1058	SKSLSLSTSQSGSTSTSTSTSASVRTSESQSTSGSMSASQSDSMSISTSFS 1108	qq	2384
ογ	755		Qy	178
Ω	1109	DSTSDSKSASTASSESISQSASTSTSGSVSTSTSLSTSNSERTSTSVSDSTSLST 1163	qq	2439
ò	812	SPSRPHYVNSTTSDLSTFESSSMNTPTSISSDGMLLSSTTLVTESET 858	Qy	238
Q	1164	SESDSISE	ą <sub>O</sub>	2490
ò	859	TTELICSDGKECSRLSSSGIVTNPDSNESSIVTSTVPTAST 900	Qy	290
q	1223	TSESVSSSTSESTSLSDSTSESGSTSTS	qq	2536
ŏ	901	MSDSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLSSSVTSLTQLSSIP 956	Οŷ	350
q	1283	LSMSTSTSLSNSTSLSTSLSDSTSDS-KSDSLSTSMSTSDSISTSKSDSISTSTSTSTST 1341	qa	2582
ó	957	SVSESBSKVTFTSNGDNOSGTHDSOSTSTELELVITSSTKV997	٥٨	402
q	1342	SESESDSTSSSESKSDSTSMSISMSQSTSGSTSTSTSLSDSTSTSLSLSASMNQSGVD 1401	ପ୍ର	2633
'n	866	LPPVVSSNTDLTSEPTNTREQPTTLSTTSNSITEDITTSQPTGDNGDNTSSTNPVPTV 1055	٥٨	441

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Homo sapidns (man)

1. Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

On: T45025

Chem. 227, 316843178, 1997

Human mucin gene MCC5B, the 10.7 kb large central exon encodes various alter con number: 222899; MUID:97166151

On: T45025

iprellminary; translated from GB/EMBL/DDBJ

signal 1.3570 Copes

et type: DNA

signal 1.3570 Copes

eferences: EMBL:272496; NID:91834502; PIDN:CAA96577.1; PID:91834503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
                                                                ATSTLASASEEDNKSGS-----HESASTSLKPSMG-ENSG-LTTSTEI-EATTTSP 1103
                                                                                                         :|| | || ::| | STSASESTSESSASTSLSUSGSASTSTSLSUSASASE 1521
                                                                                                                                                                                                                                      SDSSSTSLSDSTSASMQSSESDSQSTSASLSDSLSTSTSNRMSTIASLSTSVSTSESGST 1581
                                                                                                                                                                                                                                                                                                                         SPSTDLTSSLTT-----GTSASTSANSELVTSGSVTGGAVASASNDQSHSTSVTNSNSI 1208
                                                                                                                                                                                                                                                                                                                                                                  | || : | :| | | | | | | || || || SESTSESDSTSTSMRTSTSDSQRM 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTTTTOPVATGSMATPSSST----OTSGTPPSLITTATTITATGSTT-----NPS 2581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STPGTT-----PIPPELTTTATTP--AATSSTVTPSSALGTTHT--PPVPNTTATTHGRS 2632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSPSSPHTVRTAWTSATSCTLGTTHITEPSTGTSHTPAATTGTTTTSTPALSSPHPSSRT 2692
                                                                                                                                                                                            TEAPSPAVSSGTDVTTEPTDTREQPT----TLSTTSKTNSELVA---TTQATNENGGK 1154
   SNSASQSASNSTSTSTSESDSQSTSTYTSQSTSQSESTSTSLSDSTSISKSTSQSGST 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNDWNYPVSSES-----FSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDKTKTIEILQPIP---TTTITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTTT----- 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TVTSEWT----GTITT-----TTTRINPTDSIDTVVVQVPL---PNPTVST 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEVWSQSPATT-----TTVTAPPG--GTDTVIIREP---PNHTVTTTE-----YWS 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQF-YSGEEFTTFSTLTCTVNDAL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSSIKAFGTVT-LPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKST 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atch similarity 24.3%; Score 632.5; DB 2; Length 3570; 2a1 Similarity 24.3%; Pred. No. 1.7e-19; Indels 363; 340; Conservative 155; Wismatches 509; Indels 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B, tracheobronchial [imported] - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VSNTPQTTLSQQVT---SSSPSTNTFIASTYDGSGSI 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLSTSTSTSMSDSTSLSDSVSDSTSDSTSASTSGSMSV 1679
1402
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us-09-715-876-8.rpr

q	2693 TESPPSPGTTTPGHTTATSRTTATATPSKTRTSTLLPSOPTSAPITTVVTTGCEPOCAWS 2752	A:Reference
į	E COURTE COMMENTAL COMMENT	A; Accessio
Š	: :     : :	A; Molecule A; Residues
q	2753 EWLDYSYPMPGPSGGDFDTYSNIRAAGGAVCEQPLGLECRATAQPGVPLGELGQVVECSL 2812	A;Cross-re
οy	498 DSVIIREFAT 522	J. Biol.
qq	2813 DFGLVCRNREQVGKFKMCFNYEIRVFCCNYGHCPSTPATSSTAMPSSTPGTTWILTELTT 2872	A; ritie: J A; Referend
ò	523 TTTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSYATTTTVTAPPGGTD 570	A; Accessic A; Status:
qq		A; Molecule A; Residues
i		A, Cross-re
Ś	SYTEMEFORMINIT TEXMSQSIATITIV TAPPGGIDIVILMEPPRHINITIEMS  :	A; Accessic
ద		A;Status: A;Molecule
ò	626 QSFATTITVIGPPSGTDTVIIREPPNPTVTTEYWSQSYATTITITAPPGETDTVLIREP 685	A; Residues
	2986 KATTRATSSTSTPSSTPGTTWILTELTTAATTTAGTGPTAT 3026	A, Experime
è	686 PNHTVTTTEYWSQSYATTT-TVTAPPGETDTVLIREPPNHTVTTTEYWSQSYATTTTVTA 744	R)Toribar
Q	3027 PSSTPGTTWILTELTTTATTTASTGSTATLSSTPGTTWILTEPSTTATVTA 3077	A;Title: N
õ	EYWSQSFATT	A; Accessic
qq	3078 PPGSTATASSTQATAGTPHVSTTATTPTVTSSKATPSSSPGTATALPALRSTA 3130	A; Molecule A; Residues
ò	799 ISTSSNDITSIIPSFSRPHYVNSTTSDLSTPESSSMNTPTSISSDGMLLSSTTLVTES 856	A; Cross-re A; Note: se
q	3131 TTPTATSFTA-IPSSSLGTTWTRLSQTTTPTATMSTATPSSTPETVHTSTVLTTTA 3185	A; Note: se R; Gum, J.F
'n	857 ETTTELICSDGKECSRLSSSSGIVTNPDSNESSIVTSTVPTASTMSDSLSSTDGISATSS 916	J. Biol. C A;Title: N
g	3186 TTTGATGSVATPSSTPGTAHTTKVPTTTTTGFTATPS 3222	A;Referenc A;Accessic
ò	DNVSKSGVSVT	A; Molecule A; Residues
g		A; Cross-re A; Experime
ò	973 NOSGTHDSQSTSTEIEIVTTSSTKVLPPVVSSNTDLTSEPTNTREOPTTLSTTSNSTTED 1032	R;Jany, B
9	3262THTARVLTTTTTVATGSMATPSSSTOTSGTPPSLTTATTITAT 3306	A;Title: P
ò	17TSOPTGDNGDNTSSTNPVPTVATSTLASASREDNKSGSHESASTSLKPSMGENSGLTT	A; Accessic
7		A; Molecule A; Residues
		A, Experime
q	STATESTATISETPIPSSTLWTTWTVPAQTTTPMSTMSTIHTSSTPETTHTSTVLTTATM	Blochem. E A;Title: F
ò	BNGGKSPSTDITSSITTGTSASTSANSFIVTSGSVTGGAVASASNDOSHSTS	A; References A: Accession
3 8	TRATNSTATPSSTLGTTRILTELTTTAATGSTATLSSTPGTTMILTEPST	A; Molecule A; Residues
ò		A; Cross-re
a	IATV	A; Accessic A; Molecule
		A; Residues C; Genetics
RESULT A43932	JUL 11	A; Gene: GI
muc N, A	in 2 precursor, intestinal - human (fragments) Lternate names: mucin SMUC-41	A; Map posi C; Superfam
o o e	Decies: Homo saplens (man)  March 1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999  Annoward Annote: Antone antine, Anno 25 posts	C; Keywords F; 2766-283
ָנט פֿאַל	C.R.C.C.S.S.C.C	
₽. <b>4</b> •7	itle: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the	Best Loc

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A. Geographic number: A4993; WID:9413002
A. Geographic number: A4993; WID:9413002
A. Geographic pumps: A compared by the compa
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GDVAIDCSNIHIGITKGLNDWNYP-----VSSESFSYTKTCTSNGI---QIKYQNVP 269
                                                                             2224 TPTPSKSTPTPSKPSSTPSKPTPGT 2248
                                  1159 DLTSSLTTGTSASTSANSELVTSGS 1183
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                                                                                                               1295 LSTTPKLCCLWSDWINEDHPSSGSDDGDREPFDGVCGAPEDIECRSVKDPHLSLEQHGQK 1354
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                                                             249 SFSYTKTCTSNGIQIKYQNV-----PAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 SYLTKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTT----RTNPTDSIDTVVVQVPL 433
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                                                                                                                                                                                                LQSKP-FTLRWTGYKNSDAGSNGI-----VIVA----TTRTVTDSTTAVT----
Conservative 120; Mismatches 438; Indels 262;
Matches 285;
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hypothetical Serine/threonine repeat containing protein [imported] - fission yeast (S (S GSCE) is schizosaccherormyeas pombe (S Species Schizosaccherormyeas pombe (S Date: 03-Dec-1999 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000 (S Accession: T50375; T39173; T39174; T3936 #text_change 09-Jun-2000 (S Accession: T50375; T39173; T39174; T3936 #text_change 09-Jun-2000 (S Accession: T50375; T39172; T39173; T39174; T3936 #text_change 09-Jun-2000 (S Ascession: T50375 (S Ascession: T5
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C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosida
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A:Molecule type: DNA
A:Residues: 1-896, (26, 889-904, 1', 906-1283 <WOO>
A:Residues: 1-896, (26, 889-904, 1', 906-1283 <WOO>
A:Cross-references: EMBL:AL035675; PIDN:CAB38695.1; GSPDB:GN00067; SPDB:SPBC1289.15
A:Experimental source: strain 972h-; cosmid c1289
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A;Residues: 1-555, S' <CO4>
A;Residues: 1-555, S' <CO4>
A;Cross-references: EMBL-AL021815; PIDN:CAA17002.1
A;Cross-references: EMBL-AL021815; PIDN:CAA17002.1
A;Note: this is an interim translation for a sequence replaced by GenBank/EMBL R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Ollver, K.; Harris, D. submitted to the EMBL Data Library, March 1999
A;Reference number: 221848
A;Reference number: 221848
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A;Residues: 785-1283 <CO2>
A;Cross-references: EMBL:AL021815; PIDN:CAA17000.1
A;Note: this is an interim translation for a sequence replaced by GenBank/EMBL A;Accession: T39173
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A:Residues: 'ME',179,'PLV',183,'W','KL',556-761,'HRGSS' <CO3>
A:Cross-references: EMBL:AL021815; PIDN:CAA17001.1
A:NOTE: this is an interim translation for a sequence replaced by GenBank/EMBL
A:Accession: T99174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
8.9%; Score 578; DB 2; Length 1283;
Best Local Similarity 25.6%; Pred. No. 1.1e-17;
Matches 344; Conservative 170; Mismatches 571; Indels 258;
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RESULT 13
S57180
probable membrane protein YJR151c - yeast (Saccharomyces cerevisiae)
probable membrane protein J2223; serine/threonine-rich protein YJR151c
C:Specias: Saccharomyces cerevisiae
C:Specias: Saccharomyces cerevisiae
C:Accession: S57180
R;Scarcez, T:Aug-1995 #sequence_revision 08-Sep-1995 #text_change 05-Nov-1999
C:Accession: S57180
R;Scarcez, T:Aug-1995 #sequence Database, September 1995
A:Accession: S57180
A;Molecule type: DNA
A;Residues: 1-1161 <SCA>
A;Accession: S57180
A;Molecule type: DNA
A;Residues: 1-1161 <SCA>
A;Cross-references: EMBL:Z49651; NID:g1015902; PID:g1015903; GSPDB:GN00010; MIPS:YJR1
C:Gene: MIPS:YJR151c
A;Mop position: 10R
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 IDAYISATDVNQYTLAY-----TNDY--TCAGSRLQSKPFTLRWTGYKNSDAGSNGI 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | :: : | | ::|:| | |:
593 SEIPSSIEVLTSSGISSSVEPTSLVGPSSDESISSTESLSATSTFTSAVVSSSKAADFFT 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 IGETATVIVDVPYHTTTTVTSEWTGTITTTTTTTTTDSIDTVVVQVPLPNPTVSTTEYW 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    445 SQSFATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFATTTTVTAPPGGTDSVIIRE 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           505 PPNPTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSYATTTTVTA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 PPGGTDSVIIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVIIREPPNHTVTTTEYW 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             625 SOSFATTTTVTGPPSGTDTVIIREPPNPTVTTTEYWSQSYATTTTTAPPGETDTVLIRE 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           685 PPNHTVTTTEYWSQSYATTTTVTAPPGETDTVLIREPPNHTVTTTEYWSQ------734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       735 SYATTIV---TAPPGGIDIVIIREPPNPIVITTEYWSQ-----SFATITIVTAP 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 SSAEPTTVSEFTSSVEPTRSSQVTSSAEPT-TVSEFTSSVEPTRSSQVTSSAEPTTVSEF 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       782 PGGTDTVIIYESMSSSKISTSSNDITSIIP-----SFSRPHYVNSTTSDLSTFESSSM 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 ISSVEPTRSSQVISSAEPITVSEFISSVEPIRSSQVISSAEPTIVSEVISSVEPIRSSQV 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 IELAVYVSDIRAHIFQYYSFRNHHKTETYPSEJAAAVFDYGDFTTRLTGISGDE-----
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8.9%; Score 577; DB 2; Length 1161;
Best Local Similarity 26:3%; Pred. No. 1e-17;
Matches 299; Conservative 131; Mismatches 427; Indela 264;
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Molecule type: DNA
Residues: 1-1459 - MUNA
Cross-references: EMBL.AF024496; PIDN:AAB70340.1; GSPDB:GN00023; CESP:ZC178.2
Experimental source: strain Bristol N2; clone ZC178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein 2C178.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 29-0ct-1999
C;Accession: T32271
                                                         KVTFTSNGDNQSGTHDSQSTSTELEIVTTSSTKVLPPVVSSNTDLTSEPTNT----REQ 1018
                                                                                                                    PTTLSTTSNSITEDITTSQPTGDNGDNTSSTNPVPTV----ATSTLASASEEDNKSGSH 1073
                                                                                                                                                                               ESASTSLKPSMGENSGLTTSTEIEATTTSPTEAPSPAVSSGTDVTT--EPTDTREQPTTL 1131
                                                                                                                                                                                                                                        STTSKTNSELVATTQATNENGGKS----PSTDLTSSLTTGTSASTSANSELVTS----- 1181
                                                                                                                                                                                                                                                                                                   1182 -----GSVTGGAVASASN-----DQSHSTSVTNSNSIVSNTPQT-----TLSQQVTS 1223
                   713 AITSTSTSFIAERTSSLYLSSSNMSSFTLSTFTVSQSIVSS---FSMEPTSSVASFASSS 769
                                                                                                                                                                                                          EIVITSCKSSCTNEDSVLTKTQVSTVETTITSC-----SGGICTTLMSPVTTINAKANT 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CQFYSGEEFTTFSTLTCTV-NDALKSSIKAFGTVTLPIAFNVGGTGSSTDLEDS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTCTSNG---IQIKY 265
-SDNVSKSGVSVTTETSVTTIQTTPN-PLSSSVTSLTQ------LSSIPSVSESES 963
                                                                                                                                                                                                                                                                                                                                925 TLETTITSCSGGICTTLMSPVTTINAKANTLTTTETSTVETTITTCSGGVCSTLTVPVTT 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSTTAGPSSTATNSASSETPC ---- NSETQ --- TSDGTSTMTVPNDSTTAGPSSTATNS 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 TQTSDGTSTMT-----VPNDSTTAGPS----STATNSASSETPCNSETQTSDG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSTMTVPNDSTTAGPSSTATN-----SASSETPCNSETQTSDGTSTMTVPN 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONVPAGYRPFIDAYISA------TDVNQYTLAYINDYTCAGSRLQSKPFTLRWTG 314
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                                                                                                                                               PLLVSSRSN--CSDARSS-----NTISSGLFSTIENVRNATSTFTNLSTD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 ASSETPC---NSETQTSDGTSTMTVPNDS-----TTAGPSSTAINSASSETPCNSE
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Similarity 24.5%; Pred. No. 1.4e-16;
33; Conservative 172; Mismatches 593; Indels 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Murray, J.; Wohldmann, P.; Beck, C.
submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid ZC178.
A; Reference number: Z21143
A; Accession: T32271
                                                                                                                                                                                                                                                                                                                                                              1224 -SSPSTWTFIASTYDGSGSIIQHSTWLYGLITLLS 1257
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Gene: CESP:2C178.2
Map position: 5
(Introns: 1099/2
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Best Local Simi
Matches 333;
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S--DSTTAGPSSTVTNSASSETPCNSE-TQTSDGTSTWTVSSDSTTAGQSST-ATNSASS 1344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1231 ETPCNSETQTSDGTSTMTVPN--DSTTAGPSSTVTNSASSETPCNSETQTSDGTSTMTVS 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEIEATTTSPTEAPSPAVSSGTDVTTEPTDTREQPTTLSTTSKTNSELVATTQATNENGG 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1154 KSP-----STDLT----STDLT----SSLTTGTSASTSANSELVTSGSVTGGAVASA 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     890 IVTSTVPTASTMS-DSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLSSSVTS 948
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315 YKNSDAGSNGIVIVATTRTV-TDSTTA-----VTT-----LPFNPSV---DKTKTIEI-- 358
                                                                                                                                                                             CNSETQTSDG----TSTMTVPNDSTTAGPSSTVTNSASSETPCNSETQTSDGTSTMTVSS 461
                                                                                                                                                                                                                                                          --LQPIPTTTTTTSYVGVT-----TSYLTKTAPI-----GETATVIVDVPYHT--- 399
                                                                                                                                                                                                                                                                                                                                   DSTTPGPSSTATNSASSETPCNSETQTSDGTFTMTVSSDSTTAGPSSTVTNSASSETPCN 521
                                                                                                                                                                                                                                                                                                                                                                                                                TTTVTSEWIGTITTTTTTTTPDSIDTVVVQVPLPNPTVSTTEYWSQSFATTTTVTAP-- 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SETQTSDGTSTMTVSSDSTTPGPS-STAINSASSETPCNSET----QTSDGTSTMTVPND 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSTATNSASSETPCNSETQTSDGTSTMTVSSDSTTAGPSSTATNSASSETPCNSETQTSD 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYWSQSFATTTTVTGPPSG-TDTVIIREPPNPTVTTTEYWSQSYATTTTITAPPGETDTV 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTFTMTVPNDSTTAGPSSTVTNSASSETPCNSETQTSDGTSTMTVSNDSTTAGPSSTAT 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            681 LIREPPNHTVTTTEYWSQSYATTTTV----TAPPGETDT--VLIREPPNHTVTTTEYWS 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DTVIIYESMSSSKISTSS--NDITSIIPSFSRPHYVNSTT---SDLSTFESSSMNTPTS 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSDGMLLSSTTLVTESET--TTELICSDGKEC-----SRLSSSSGIVTNPDSNES--S 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- NSASSETPCNSETQTSDGTFTMTVPNDSTTAGPSSTATNSASSETPCNSETQTSDGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  734 QSYATITIVTAPPGGTDT--VIIREPPNPTVTTTEYWSQSFATTTTVTAPPGGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       874 TMTVPNDSTTAGPSSTATNSASSETPCNSETQTSDGTSTMTVPNDSTTAGPSSTATNSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           577 STTAGPSSTATNSASSETPCNSETQTSDGTSTMTVPNDSTTAGPSSTVTNSASSETPCNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      637 ETQTSDGTSTMTVSSDSTTAGPSSTATNSASSETPCNSETQTSDGTSTMTVSSDSTTAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PGGTDT--VIIREPPNHTVTTTEYWSQSFATTTTVTAPPGG---TDSVIIREPPNP
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1148 QTSIQYTLSTATTISGLKTVYTWCPLTSKSTLGATTQTS-----STAKVRITS-AS 1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SATSTSISLSTSTESE----SSSGYLSKGVCSGTECTQDVPTQSSSPASTLAYSPSVSTS 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSITEDITTSQPTGDNGDNTSSTNPVPTVATSTLASASEEDNKSGSHESASTSLKPSMGE 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1088 SSSTPSQYSLSTATTTINGIKTVYTTWCPLAEKSTVAASSQSSRSVDRFVSSSKPSSSLS 1147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRSTPFPYLTSSTSSSSLASTKKSSL-----EASSEMSTFSVSTQSLPLAFTCS 1037
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                                                                                                                                                                                                                                                    921 KSGVSVTTETSVTTIQ-----TTPNPLSSSVT--SLTQLSSIPSVSESESKVTFTSNGD 972
                                                                                                                                                                                                                                                                                                                                                                                                           683 REPPNHIVITIEYWSQSYAITIIVIAPPGEID ---IVLIREPPNHIVITIEYWSQSYAI 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSTASETIST -- LGTONFTTTGSLLFPALSTEMINTTVVSRKT--- LIISTEVCSHSKCV 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        739 TTTVT-----APPGG-----TDTVIIREPPNPTVT-TTEYWSQSFATTTTVTAPPG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     930 PTVITEVVTSKGTPSNGHSSQTLQTEAVEVTLSSHQTVTMSTEVCSNSICTPTVITSVQ- 988
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                                                                                                                                                 623 YWSQSFATTTTVTGPPSGTDTVIIREPPNPTVTTTEYWSQSYATTTTTAPPGETDTVLI 682
                                                                                                                                                                                                                                                                                                                                                            GAKNPAASEVIINTOVSATS-----EATSTSTQ-----VSATSATATASESSTTSQ 874
                         --PPGGTDSVIIREPPNPTVTTTEY
                                                     WSQSFATTTTVTAPPGGTDSVIIREPPNPTVTT----TEY--W--SQSYATTTTVTAP
                                                                                                                                                                                                               566 PGCTDSVIIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVIIREPPNHTV---TTTE
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Job time: 252 sec
                         NHTVT - - - TTEYWSQSFATTTTVTA - - -
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Yast 8, 569-575, 1992
A:Title: The complete sequence of a 6146 bp fragment of Saccharomyces cerevisiae chromos
A:Reference number: S25345; MUID:92397594
A:Accession: S25345
                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
Sesdides: 1-1609 CWLL>
Grassides: 1-1609 CWLL>
Grassides: GB: X59720; EMBL: S43845; NID: g1907116; PIDN: CAA42254.1; PID: g1907227
Frontall, L.; Grisantl, P.
Frontall, L.; Grisantl, P.
Reference number: S19504
Accession: S19504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #:Molecule type: DNA
A:Residues: 1-1609 <FRO>
A:Cross-references: EMBL:X59720; NID:91907116; PID:e264634; PID:91907227; MIPS:YCR089w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                probable membrane protein YCR089w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YCR1102
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C;Accession: $25345; $19504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 SLTFTSVNPSQSWTSFNSE---KSSALSSTIDFTSSEISGSTSP-KSLESFDTTGTITSS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRSSSMAPTSGSDSISHNFTSPPSKTSGNYDV-----LTSNSIDPSLFTTTSEYSSTQLS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 VNDA-----GTVTLPIAFNVGGTGSST 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 YSPSPSSKNSNQTSLLSPLEPLSSSGDLILSSTIQATTNDQTSKTIPTLVDATSSLPPT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 IHIGITKG---LNDW---NYPVS-------SESFSYTKTCTSNGIQI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQYQDWSSSSLPLSQTTWVVINTINTQGSVTSTTSPAYVST-ATKTVDGVITEYVTWCPL 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 DLEDSKCFTAGTNTVTFN-----DGDKDISIDVEFEKSTVDPSAYL----YASRVMP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KY-----QNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EYVIWCPLTQTKSQAIGVSSSISSVPQASSFSGSSILSSNSSTLAAS--NNVPESTASGS 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTITTSYVGVTTSYLTKT-----APIGETATVIVDVPYHTTTTVTSEWTGTITTTT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           573 TQTKSQAIGISSSTISATQTSKPSSILTLGISTLQLSDATFKGTETIN---THLMTESTS 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTNPT-----DSIDTVVVQVPLPNPTVSTTEYWSQSFATTTVTAPPGGTDTVIIREPP 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLNKVT---------TLFVAPQCENGYT-SGTMGFSSSNGDVAIDCSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.4%; Score 547.5; DB 2; Length 1609; Best Local Similarity 22.5%; Pred. No. 3e-16; Matches 332; Conservative 232; Mismatches 503; Indels 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: SGD:PIG2
A;Cross=references: SGD:S0000685; MIPS:YCR089w
A;Map postition: 3R
C;Keywords: transmembrane protein
E;4-20/Domain: transmembrane #status predicted <TMI>
F;1592-1609/Domain: transmembrane #status predicted <TMI>
1405 STTAGQSSTATNSAS -- SETPCNSETQ -- TSDKTSTMTF 1439
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homo sapien
homo sapien
saccharomyc
gallus gall
bos taurus
xenopus lae
haemophilus
homo sapien
                                                                                                                                                                                                                                             rattus norv
                                                                                                                                                                                                                                                                         saccharomyc
candida alb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enkaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TAXID-5476;
P35658
P13611
P40442
P40442
P61282
Q005049
P45386
Q99102
P52591
P52591
P56591
P38739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat; Signal.
POTENTIAL.
AGGLUTININ-LIKE PROTEIN 1.
10, X 36 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 40, Last annocation update)
Agglutinin-like protein 1 precursor.
ALS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1260 AA.
N214_HUMAN
PCC_HUMAN
Y109_YEBC
PGCV_CHICK
PGCV_CHICK
PGCV_BOVIN
MUC1_XEBLA
MUC1_XEBLA
MUC1_HUMAN
N121_KAT
YNR6_YEBAT
HYR1_CANAL
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Cell adhesion; Glycoprotei
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensetisb-sib.ch).
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                      PPGGTDTVIIYESMSSSKISTSSNDITSIIPSFSRPHYVNSTTSDLSTFESSSMNTPTSI
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Bukaryota: Fungi: Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID-5476;
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-!- FUNCTION: MAY PLAR A ROLE IN ADHESION AND PATHOGENESIS.
-!- PTW: N-GLYCOSYLATED AND O-GLYCOSYLATED (POTENTIAL).
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MEDLINE-98309840; PubMed-9644209;
Hoyer L.L., Payne T.L., Bell M., Myers A.M., Scherer S.;
"Candida albicans ALS3 and Insights into the nature of th
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ALS3
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Cell adhesion; Glycoprotein; Repeat; Signal.
SIGNAL 17 POTENTIAL.
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1039 -----SSPSTTTTANNDSVITG------TTSTNQSQSQYN-----SDTQQTTLSQ 1080
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15-50L-1999 (Rel. 38, Last sequence update)
15-50L-1999 (Rel. 38, Last annotation update)
15-50L-1999 (Rel. 38, Last annotation update)
Agglutinin-like protein ALAI precursor (Agglutinin-like adhesin).
Adglutinin-sike protein ALAI precursor (Agglutinin-like adhesin).
Candida albicans (Yeast).
Candida albicans (Yeast).
Saccharomyceties; mitosporic Saccharomyceties;
Saccharomyceties; mitosporic Saccharomyceties;
NCBL_TAXID-5476.
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SEQUENCE FROM N.A.
MEDLINE-98053977; PubMed-9393828;
Gaur N.K., Klotz S.A.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the ENBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licensediab-sib.ch).
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"Expression, cloning, and characterization of a Candida albicans gene, ALAI, that confers adherence properties upon Saccharomyces cereevisiae for extracellular matrix proteins."; Infect. Immun. 65:2809-2804(1997).

1- FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.

1- PTM: N-GLYCOSYLATED AND O-GLYCOSYLATED (POTENTIAL).
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DD 1369 ASNSQPTTLIQQVATS--SYNQPLITTYAGSSSATKHPSMI
RESULT 4
ALS2\_CANAL
ID ALS2\_CANAL
STANDARD; PRT; 468 AA.
AC 074657;
DT 15-UUL-1999 (Rel. 38, Created)
DT 15-UUL-1999 (Rel. 38, Last sequence update)

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CANAL
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SEQUENCE
    RESULT 5
ALS4_CANAL
ID ALS4_CA
AC 074660;
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                                                                                                                                                                                 STRAIN-1161;

RX MEDINE-88440404. Pubmed-9765564;

RX MEDINE-88440404. Pubmed-9765564;

RY Hoyer L.L., Payne T.L., Hecht J.E.;

RY HOYER T.L., Payne T.L., Hecht J.E.;

RY HOSE T.L., Payne T.L., Hecht J.E.;

RY HOYER T.L., Payne T.L., Hecht J.E.;

RY HOYER T.L., HE T.L., HEL
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Kakaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TAXID-5476.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 30.7%; Score 1992.5; DB 1; Length 468; Best Local Similarity 80.2%; Pred. No. 1.2-79; Matches 376; Conservative 33; Mismatches 59; Indels 1;
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50203 MW; BFE773E169ED0FAF CRC64;
15-JUL-1999 (Rel. 38, Last annotation update)
Agglutinin-like protein 2 precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AF024580; AAC64235.1; -- Cell adhesion; Glycoprotein; PoTENTIAL.
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253 2
315 3
468 4
                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDILINE-98440424; PubMed-9765564;
MEDILINE-98440424; PubMed-9765564;
HOVET L.L., Payne T.L., Hecht J.E.;
"Identification of Candida albicans ALS2 and ALS4 and localization of als profesins to the fungal call surface.";
J. Bacteriol. 180:5334-5343(1998).
-I- FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.
-I- PIM: N-GLYCOSYLATED AND O-GLYCOSYLATED (POTENTIAL).
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                                                                                                                                                                                                                                           Ebkaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_maxID-6476.
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28.0%; Score 1819; DB 1; Length 469;
Best Local Similarity 72.1%; Pred. No. 3.7e-72;
Matches 338; Conservative 48; Mismatches 83; Indels
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SIGNAL 1 17 POTENTIAL.
CHAIN 18 >469 AGGLUTININ-LIKE PROTEIN 4.
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469 AA; 49604 MW; OEDCAB19B89EFCB1 CRC64;
                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Agglutinin-like protein 4 precursor (Fragment).
469 AA.
PRT;
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STANDARD;
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SEQUENCE FROM N.A.
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**REDLINE-942623153; PubMed-8203162;

**MEDLINE-942623153; PubMed-8203162;

**MEDLINE-942623153; PubMed-8203162;

**Alexation U. Jaatinen R., Penttilae M., Keraenen S.;

**Alexation U. Jaatinen R., Penttilae M., Keraenen S.;

**Alexation II-226(1994).

**The modecular cloning and analysis of the yeast flocculation gene FLOI.";

**Part 10:211-226(1994).

**The modecular cloning and analysis of the yeast flocculation gene FLOI.";

**Part 10:211-226(1994).

**Sauth 10:211-226(1994).

**Sauth 10:211-226(1994).

**Sauth 10:211-226(1998).

**Alexation No. Alexation N
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MEDLIME-9328981; PubMed-8511970;
Teunissen A.W.R.H., Holub E., van der Hucht J., van den Berg J.A.,
Steensma H.Y.;
"Sequence of the open reading frame of the FLO1 gene from
Saccharomyces cerevisiae.";
Yeast 9:423-427(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomyceteles;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID-4932;
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1 24 POCTENTIAL, SIGNAL 25 PLOCCULATION PROFEE FLOX.
CHAIN 25 PROPEP PROVED IN MATURE FORM (POTENTIAL).
01-OCT-1993 (Rel. 27, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Flocculation protein FLO1 precursor (Flocculin 1).
FLO1 OR YAR050W.
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--- PPM: EXTRNSIVELY O-GLYCOSYLATED (PROBABLE).
--- SIMILARITY: BELONGS TO THE FLOCCULIN FAMILY.
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FLOL_YEAST
P32768;
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<b>КЕРЕАТ</b>	REPEATS.  TIAL).	# 1; Length 1537;  # 523; Indels 418; G
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POXIM	XIMA  XIMA  COLUMN  CO	1; 33; 523; 131; 142; 152; 152; 153; 173; 174; 175; 175; 175; 175; 175; 175; 175; 175
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2	* 000000000000000000000000000000000000	B 940; D ismatches  TGVFDSF : : :
7	11-18. 2	tch 14.5%; Score 940; DB 1; Length 1537; al Similarity 26.0%; Pred. No. 1.1e-33; 417; Conservative 244; Mismatches 523; Indels 418; G LQOFTLLFLYLSIASAKTITGVFDSFNSLTWSNAANYAF LAVFTLLAL-TSVASGATEACLPAGOREGOMINYQYSLESSTYSMANAMAGYASKT LAAVFTLLAL-TSVASGATEACLPAGOREGOMINYQYSLESSTYSMANAMAGYASKT LAAVFTLLAL-TSVASGATEACLPAGOREGOMINYQYSLESSTYSMANAMAGYASKT LSANPGDTFTLNM
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InterPro; IPR001389; Flocculin.
Pfam; PF00624; Flocculin; 13.
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                    251 SYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTL 310
                                                                                356 -----IEILQPIPTTTTT-----SYVGVTTSYLTKTA----PIGETATVIVDVPYH 398
                                                                                                                       439 PTDETIIVIRTPTTATTAMTTTQPWDDTFTSTSTEMTTVTGTNGLPTDET-IIVIRTPTT 497
                                                                                                                                            TTT--TVTSEWTGTIT-----TTTTRIN--PTDSIDTVVVQVPLPNPT-VSTTEYWSQS 447
                                                                                                                                                                                    448 FATT----TTVTAPPG-GTD--TVIIREPPNHT--VTTTEYWSQSFATT----TTVTAPP 494
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278 TTTEPWTGTFTSTSTEMTTVTGTNGVPTDETVIVIRTPTTASTIITTTEPWNSTFTSTST 337
                                        ELTIVICINGVRIDETII-----VIRTPITATIAITTEPWNSTFTSTSTEL----- 384
                                                           311 RWTGYKNSDAGSNGI---VIVATTRTVTDSTTAVTTL-PFNPSVDKTKT------
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-----QATNENGGKSPSTDLTSSLTTGT-SASTSANSELVTSGSVTGGA 1188
                                       1375 TATVNDVVTVYPTWRPQTANEESVSSKMNSATGETTTNTLAAETTTTNTVAAETITNTGAA 1434
                                                                                                                                                                                1435 ETKTVVTSSLSRSNHAETQTASATDVIGHSSSVVSVSETGNTKSLTSSGLSTMSQQPRST 1494
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SEQUENCE FROM N.A.
STRAIN-$238G / AB972;
STRAIN-$5248G / AB972;
STRAIN-$5248G / AB972;
MEDLINE-$5249G / BUBMC4-7731988;
BUSSEY H., Kabback D.B., Zhong W., Vo. D.T., Clark M.W., Fortin N., Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K., Storms R.K.;
Storms R.K.;
"The nucleofide sequence of chromosome I from Saccharomyces "The nucleofide sequence -- "19489-3813(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FBB-1995 (Rel. 31, Created)
1-FBB-1995 (Rel. 33, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
Hypothetical 138.1 kDa protein in FLO9-GBH3 intergenic precursor.
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Makaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; NCBL_TaxID-4932;
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Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
-1- SIMILARITY: STRONG, TO YEAST PROTEIN FLOI.
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                                                                                                                                                                                                                                                                                        259 SQPNCTIPDDSNYTVSTTITTTEP----WTGTFTSTSTEMTTVTGTNGVPTDETVINIRT 314
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                                                                                                                                                                                                                                                199 SPPDNITGTVYMYAGFYYPMKIVYSNAVAWGTLPISVTLPDGTTVSDDFEGYVYTFDNNL 258
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                                              NSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFKYTTSQT----S 83
                                                             542 TATTAMITIQPWNDTFTSTSTEMTTVTGTNGLPTDETIIVIRTPTTATTAITTEPWNST
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Ouery Match
14.4%; Score 932.5; DB 1; Length 1322;
Best Local Similarity 28.1%; Pred. No. 2e-33;
Matches 400; Conservative 215; Mismatches 468; Indels 339;
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                                                                                                                               LSSIPSVSESESKVTFTSNGDNQSGTHDSQSTSTELEIVTTSSTKVLPPVVSSNTDLTSE 1011
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                                                           949 SSVIPTSSSTSGSSESETGSASSAS---SSSSISSESPKSTYSSSSLP-PVTSATTSQEI 1004
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BIOLINE-93016075; PubMed-1400449; N., Rothe E.-M., Lagace R.E.,
Gum J.R. Jr., Hrks J.W., Toribara N.W., Rothe E.-M., Lagace R.E.,
Kim Y.S.,
The human MUC2 intestinal mucin has cysteine-rich subdomains located
both upstream and downstream of its central repetitive region.";
J. Biol. Chem. 267:21375-21383(1992).
892 TSTVPTASTMSDSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLSSSVTSLTQ 951
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                                                                                                                                                                                                                                                               1012 PT---NTREQPTTLSTTSNSITEDIT-TSQPTGDNGDNTSSTNPVPTVATSTLASASEED
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Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TAXID=9606;
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SEQUENCE OF 626-1895 AND 4196-5179 FROM N.A.
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11.1%; Score 721.5; DB 1; Length 5179;
Best Local Similarity 25.3%; Pred: No. 1.1e-23;
Matches 335; Conservative 118; Mismatches 554; Indels 279;
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                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            - 1 SUBCELLULAR LOCATION: Secreted.
- 1 TISSUE SPECIFICITY: COLON, SMALL INTESTINE, COLONIC TUMORS,
- 1 TISSUE SPECIFICITY: COLON, SMALL INTESTINE, COLONIC TUMORS,
- 1 FTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
- 1 TISCHAIN DISGULFIDE BOONDS (BY SIMILARITY).
- 1 FOLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND
- 1 SIMILARITY: THE N-TERMINAL DOMAINS SOME SIMILARITY TO THAT
- 1 SIMILARITY: CONTAINS 2 VWFC DOMAINS.
- 1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
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PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01208; VWFC; 2.
Glycoprotein; Repeat; Signal.
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InterPro: IPR000561; EGF-11ke.
InterPro: IPR001007; VWRC.
InterPro: IPR001007; VWRC.
Pfam: PF00007; Cys_knot; 1.
Pfam: PF00094; VWd. 4.
PRINTS; PR00138; GFCYSKNOT.
SWART; SW00214; VWC; 2.
SWART; SW00216; VWC; 4.
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EMBL; M74027; AAA59875.1; -
EMBL; M94131; AAA59163.1; -
EMBL; M94132; AAA59164.1; -
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                                                             536 VIIREPPNPTVTTTEYWSQSYATTTTVTAP---PGGTDSVIIREPPNHTVTTTEYWSQSY
                                                                                        2333 TITIVIPIPIPICIOIPITIPITITITIVIPIPIPICIOI-----PITIPITITI-----
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 33, Last annotation update)
Floculation protein FLOS precursor (Flocculin 5).
FLOS OR YHEXILW.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                            STRAIN-S288C / AB972;
MRDLINE-94378003; PubMed-8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jler M., Johnston L., Langston Y.,
Lafreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 AGTNTVTFNDGDKDISIDVEF ----- EKSTVDPSAYL --- YASRV----- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 -- MPSLNKVTTLFVAPQCENGYTS-GTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 SESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSR---L 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 IDLFGFYTTPINVTLEMTGYFLPPQTGSYTFSFATVDDSAILSVGGSIAFECCAQEQPPI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 OSKPFTLRWTGYKNSDAGSNGIVIVATT------RTVTDSTTAVTTLPFNPSVDKT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                            23 SGATEACLPAGORKSGMNINFYQYSLKDSSTYSNAAYMAYGYASKTKLGSVGGQTDISID 82
                                                                                                                                                                                                                             "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECOCCULATION PROTEIN FLOS.
REMOVED IN MATURE FORM (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
M-LINKED (GLCNAC...) (POTENTIAL).
MM; DISIB370BGOGBDSF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.9%; Score 711; DB 1; Length 1075; 11arity 25.9%; Pred. No. 5.56-24; Conservative 192; Mismatches 393; Indels 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Membrane; Repeat; Cell wall; Signal; GPI-anchor.
SIGNAL 1 24 POTENTIAL.
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential).
-- PPM: EXTENSIVELY O-GLYCOSYLATED (PROBABLE).
-- SIMILARITY: BELONGS TO THE FLOCCULIN FAMILY.
                                                                                                                                                                                                                                                                                                              MEDLINE-96076625; PubMed-7502576;
Teunissen A.W., Steensma H.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U00029; AAB69731.1; -. PIR; 848992; 848992. SCD: S0001254; FLO5. InterPro; IPR001389; Flocculin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111981 MW;
                                                                                                                                                                                                                                                             Science 265:2077-2082(1994).
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187
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1075 AA;
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                                                    SEQUENCE FROM N.A
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Pfam; PF00624;
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Matches 324;
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CARBOHYD
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979 TSSLSRFNHAETQ------TASATDVIGHSSSVVSVSETGNTMSLTSSGLS 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1108 ··SPAVSSGTDVTT-----EPTDTREQPTTLSTTSKTNSELVATTQATNENGGKSPSTDL 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1161 TSSLTTGTSASTSANSELVTSGSVTGGAVASASNDQSHSTSV----TNSNSIVSNTPQT 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNPVPTVATSTLASASEEDNKSGSHESASTSLKPSMGENSGLTTSTEIEATTTSPTEAP- 1107
                                                                                                                                                                                                                                                                                                                                                      WSQSFATT----TTVT----GPPSGTDTVIIREPPNPTV--TTTEYWSQSYATT----TTI 670
                                                                                                                                                                                                                                                                                                                                                                         641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCIVINPDSNESSIVISTVPTASTMSDSLSSTDGISATS----SDNVSKSGVSVTTET 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         754 LPPVISATIGGET -- ASSLPPATITKTS - EQITLVIVISCESHVCTESISSAIVSTATVT 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       931 --SVTTIQTTPNPLSSSVTSLTQLSSIPSVSESESKVTFTSNGDNQSGTHDSQSTSTEIE 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               848 TETTKQTTVV-TISSCESDICSKTAS----PAIVSTSTATI------NGVTTEY 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     926 IVSTATATVNDVVTVYPTWRPQTINEQ----SVSSKMNS---ATSETTINTGAAETKTAV 978
                                                                                                                                                                                                                                             TAPPGE-TD--TVLIREPPNH--TVTTTEYWSQSYATT----TTVTAPPGE-TD--TVLI 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPPNH--TVTTTEYWSQSYATTTTVTAPPGGT-----DTVIIREPPNPTVTTTEYWSQ 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPATTTTVTA------PPGGTDTV---IIYESMSSSKISTSSNDITSIIPSFSRPHY 818
                                                                                                                                                            464 VIIREPPNHTVTTTEYWSQSFATT ---- TTVTAPPG-GTDS--VIIREPPNP--TVTTE 514
                                                                                                                                                                                  YWSQSFATT----TTVTAPPG-GTDS--VIIREPPNP--TVTTTEYWSQSYATTTTVTAP 565
                                                                                                                                                                                                                                                                                        PGGTDSVIIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVIIREPPNH--TVTTTEY 623
184 TSTNFTI--NGIKPWD-GSLPDNITGTVYMYAGYYYPLKVVYSNAVSWGTLPI--SVE-- 236
                                                                                                                354 KTIEILQPIPT-TTITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTT---TTVTSEWTG
                                                      410 TIT-----TTTTRTNPTDSIDTVVVQVPLPNPTVSTTEYWSQSFATTTVTAPPGGTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1216 TLSQQVTSS-----SPSTNTFIASTYDGSGSIIQHSTWLYGLITLLSLFI 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1024 TWSQQPRSTPASSWVGSSTASLEISTYAGSANSLLAGSGLSVFIASLLLAI 1074
                                                              237
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EMBL: 228061; CAA86176.1;

EMBL: AAA35014.1;

EMBL: Mid164; AAA35015.1;

EMBL: Mid165, AAA35015.1;

EMBL: Mid165, AAA35015.1;

EMBL: Mid164: AAA35015.1;

EMBL: AAA350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-31 FROM N.A.
STRAIN-SPAIO1-1C;
MEDLINE-89031230; PubMed-3141213;
MEDLINE-89031230; PubMed-3141213;
Pardo J.M., Ianez E., Zalacain M., Claros M.G., Jimenez A.;
"Similar short elements in the 5' regions of the STA2 and SGA genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-242 AND 762-1331 FROM N.A.
BUDIND-87194660; PubMed-3106330;
Yamashita I., Nakamura M., Fikui S.;
"Gene fusion is a possible mechanism underlying the evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polysaccharide degradation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                               TRAIN-SERBE / AB972;
BATRAIN-SERBE / AB972;
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser / Gentles S., Hamlyn N., Bornenll T.S., Hunt S., Jagels K., Jones / Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Wafandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S., Wolle E., Moule T., Genbank/DDBJ databases.
                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Kanglis Fungl; Ascomycota; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; NCBL_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
GLÜCOAMTALS SI/S2.
SER/THR-RICH.
N-LINKED (GLCNAC...) (POTENTIAL)
MW. 91CODEZDBOGIAN9D CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1367;
                                                       01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
61ucoamylase S1/62 precurence (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase) (1.4-alpha-D-glucan glucohydrolase).
STA1 OR STA2 OR MALS OR YIR019C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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10.4%; Score 675.5; DB 1;
Best Local Similarity 26.2%; Pred. No. 2.5e-22;
Marches 349; Conservative 177; Mismatches 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 169:2142-2149(1987).
            P08640; P08068;
01-AUG-1988 (Rel. 08, Created)
01-FEB-1995 (Rel. 31, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136110
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Signal, Multigene family.
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1367 AA;
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RESULT 10 AMYH\_YEAST

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Gaps

Indels 353;

Fri Oct 4 08:13:48 2002

Oy Oy	1 MLQOFTLLFLYLSIASAKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTS 60   1   1   1   1   1   1   1   1   1
Db Qy 1	37 CNSIVNGCPNLDFNWHMDQQNIMQYTLDVTSVSWVQDNT-YQITIHVKGKE 86  113 TVNDALKSSIKAEQTVTLPIAFNVGGTGGSPTLEDSKC-FTAGTNTVYFN-DGDKDI- 167
	NIDLKYLWSLKIIGVTGPKGTVQLYGYNENTYLIDNPTDFTAFEDYATQDVNSIDVBFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSN
6 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	140 SCQVWMPNFQIQFEYLGGSAAQYASSMQWGFTSFDLST 177  221 GDVAIDCSNIHIGITKGLNDMNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYI 280  178 GNNYD
	SATDVNQYTLAYTNDYTGAGSKPTLRWTGYKNSDGSNGIVLVATTRTVTDSTTA
0y 3	341 VTTLPENPSVDKTKTIEILQPIPTTITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTT 400
0y 4 0b 2	401 TTVTSEWTGTITTTTRNPTDSIDTV-VVQVPLPNPTVSTTEKWSQSFATTTV 454                                 293 TPCTKKKTTTSKTCTKKTTTPVPTPSSSTTESSSAPVTSTTESS
Oy 4 Db 3	455 TAPPGGTDTVIIREPPNHTVTTEYWSQSFATTTTVTAPPGGTDSVIIREPNPTVT 511 : : : : : : : : : : : : : : : : : :
Oy 5 Db 4	512 TTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSYATTTT-VTAPPGGTD 570 
Oy 5 Db 4	571 SVITREPPNHTVTTTEYMSGSYATTTTVTAPPGGTDTVIIREP-PNHTVTTTE 622 
Oy 6 Db 5	623 XMSOSFATTTTVTGPPSGTDTVIIREP-PNPTVTTTEYMSQSYATTTTITAPPGE 676
2 6	677 TDTVLIREPPNHTVITTEYMSQSYATTTTVTAPPGETDTVLIREPPNHTVTTTE 730 : : :   :
Oy 7 Db 6	731 YMSQSYATTTTVTAPPGGTDTVIIREP-PNPTVTTFYWSQSFATTTTVTAP 781 
Oy 7 Db 6	782 PGGTDTVIIYESMSS8KISTSSNDITSIIPSFSRPHYVNSTTSD 825 
Oy 8 Db 7	826LSTFESSSMNTPTSISSDGMLLSSTTLVTESETTTELICSDGKECSRLSSSGIVTN 882 
Qy 8 Db 8	883 PDSNESSIVTSTVPTASTMSDSL-SSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNP 941   I   I   I   I   I   I   I   I   I   I
Oy 9 Db 8	942 LSSSVTSLTQLSSIPSVSESESKVTFTSNGDNQSGTHDSQSTSTEIEIV 990     :
6 AO	991TISSTKVLPPVVSSNTDLTSEPTNTREQPTTLSTTSNSITEDITTSQP 1038

qq	
Qy	1039 TGDNGDNTSSTNPVPTVATSTLASASEEDNKSGSHESAST 1078
qq	990 TGTNSAGETISGCSP-KTITTIVPCSISPSETASESTTTSPTTPVTTVVSTTVVTTEYST 1048
oy	SLKPSMGENSGLITS-TEIBATITSPTBAPSPAVSGTDSGTD
g	STRPG-GEITTTFVTKNIPTTYLTTIAPTPSVTTVTNFTPTIITTVCSTGINSAGE
δ δ	1117VTTEPTDTREQPTTLSTTSKTNSELVATTQATNENGGKSPSTDLT 1161
ò	SELTETETSASTSANSELVISGSVIGGAVASASNDOSHSISVINGNSIVSN
7 d	:: :  :                    ::   :   :
Qy	1212TPQTTLSQQVTSSSPSTN
qa	1224 ENTAPSATTPVTTAIPTTVITTESSVGTNSAGETTTGYTTKSIPTTYITLIPGSNGAKN 1283
Qy	1245 HST 1247
qq	1284 YET 1286
RESULT DAN4_Y ID D	ILT 11 LYEAST STANDARD: PRT: 1161 AA.
	01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update)
	01-MAR-2002 (Rel. 41, Last annotation update)
	DANA OR YURISIC OR J2223.
	Saccharomyces cerevisiae (Baker's yeast). Eukarvota: Fundi: Ascomycota: Saccharomycotina: Saccharomycetes:
	ccharomyces.
	NCB1_TBXID#4932;
RP.	SEQUENCE FROM N.A.
R. R.	Scarcez r.; Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
RN	
A X	KEGULATION. MEDIJINE-21113168: PubMed-11160904:
RA	Cohen B.D., Sertil O., Abramova N.E., Davies K.J., Lowry C.V.;
RT	"Induction and repression of DANI and the family of anaerobic mannoprotein genes in Saccharomyces cerevisiae occurs through a
RT	•
3 S	TEIC ACIDS RES. 29:795-808(2001). FUNCTION: COMPONENT OF THE CELL WALL (By similarity)
ខ្ល	brane b
88	PTM:
ည	-!- SIMILARITY: BELONGS TO THE SRP1 / TIP1 FAMILY.
ម	This SWISS-PROT entry is copyright. It is produced through a collaboratio
႘႘	between the Swiss Institute of Bioinformatics and the EMBL outstation
38	use by non-profit institutions as long as its content is in no wa
88	modified and this statement is not removed. Usage by and for commercia
38	se dyreement (see nttp://www.rsb se@lsb-sib.ch).
ပ္ပ ၕ	EMB1: 249551: CAA89684.1: -
DR	3912; DAN4.
DR DR	Interpro; IPR000992; SRP1_TIP1. Pfam: PF00660; SRP1_TIP1: 1.
DR	TE; PS00724; SRP1_TIP1; 1.
ΚW	Cell wall; Glycoprotein; Membrane; GPI-anchor; Signal.

Db 813 EIVITSCKSSCTNEDSVLTKTQVSTVETTITSCSGGICTTLMSPVTTINAKANT 866  QY 1132 STTSKTNSELVATTQATNENGEKSPSTDLTSSLTTGTSASTSANSELVTS 1181	TEAST STANDARD; PRT; 1609 AA.  33:  13:  13:  14:1992 (Rel. 22, Created)  14:1992 (Rel. 22, Last sequence update)  15:1999 (Rel. 27, Last annotation update)  15:1990 (Rel. 37, Last annotation update)  15:1991 (Rel. 37, Last annotation update)  16:1991 (Rel. 37, Last annotation update)  16:1992 (Rel. 37, Last annotation update)  16:190 (Rel. 38, Leavendry update)  17:190 (Rel. 38, Leavendry update)  17:190 (Rel. 38, Leavendry update)  18:190 (Rel. 38, Leavendry update)  18:190 (Rel. 38, Leave	Db 281 LRSSSMAPTSGSDSISHNFTSPPSKTSGNYDVLTSNSIDPSLFTTTSEYSSTQLS 335 Qy 192 SLNKVT
FT SIGNAL 1 24 POTENTIAL. FT CHAIN 25 1146 CELL WALL PROTEIN DAN4. 25 1146 CELL WALL PROTEIN DAN4. 26 1147 1161 REMOVED IN MATURE PORM (POTENTIAL). 27 FT LIPID 1146 1146 CPI-ANCHOR (POTENTIAL). 28 SEQUENCE 1161 Aa; 118358 MW; 7954C15D69F0CA58 CRC64; 29 SEQUENCE 1161 Aa; 118358 MW; 7954C15D69F0CA58 CRC64;  OWERY MATCh  BASI LOGAL SIMILARITY 26.3%; Pred. No. 3.6e-18; BASI LOGAL SIMILARITY 26.3%; PRED. No. 3.6e-18; BASI LOGAL SIMILARITY 1161; BASI LOGAL SIMILARITY 1161; BASI LOGAL SIMILARITY 1161; BASI LOGAL SIMILARITY POSETARAN FORTREND GROWN 1325 1: :1: :1: :1: :1: :1: :1: :1: :1: :1:	VIVATTRIVTOSTTAVTILPENDSVDKTKTIE-ILQPIPTTITITSVGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Qy         1019         PTTLSTTSNSITEDITTSQPTGDNGDNTSSTNPVPTVATSTLASASEEDNKSGSH 1073             1   1   1   1   1   1   1   1   1   1

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qq	456 EYVTWCPLTOTKGAIGVSSISSYPOASSFSGSTISSANSTLAASNNVPESTAGG 513	Up 1423 TCTGSECQNTTSSSCDGISCN
		QY 1211 NTPQTTLSQQVTSSSPSTNT
ò	315 YKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPT 364	:     :      : 
q	514 SQYQDWSSSSLPLSQTTWVVINTTNTQGSVTSTTSPAYVST-ATKTVDGVITEYVTWCPL 572	
Oy	365 TIITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTTTVTSEWTGTITTTT 416	RESULT 13
ż		96_YEAST
g G	5/3 TQTKGQALGLSSSTLSATQTSKPSSLLTLGLSTLQLSDATFKGTETINTHLMTESTS 529	
ò	417 RINPTDSIDTVVVQVPLPNPTVSTTEYWSQSFATTTTVTAPPGGTDTVIIREPP 470	
ç	630 THEPTOGENET CHEST III IIII IIII IIII IIII IIII IIII II	
1		DE Hypothetical 113.1 kDa prot
	471 NHTVTTTEYMSQSFATTTTVTAPPGGTDSVIIREPPNPTVTTEY 515	
ŝ	674 NSTVTFGSTSKYPSTSVSNPTEASQHVSSSVNSLTDFTSNSTETIAVISNIHKTSSNKDY 733	OC Eukaryota; Fung1; Ascomycot
ò	516 WSOSFATTITVTAPPGGTDSVIIREPPNPTVTITEYWSOSYATTITVTAP 565	
1 4		
3	SELTIQEATSGAQIEVESIVITIVNGARIEXTIMCPASSLAXITISISI	
οy	566 PGGTDSVIIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVIIREPPNHTVTTTE 622	
qq	782KTLVLTTEVCSHSECTPTVITSVTATSSTIPLLSTSSSTVLSSTVSE 828	CC -1- DOMAIN: CONTAINS MANY S
	623 VUSASDAMMHINIMCDDSCAMDHILTDDDDNIPHIHMHIDVISASAVAMHHIMADDCICAMDHILT 602	
ŝ	INSUSTRAITITYTGPPSGIDIVITREPPNPIVITIEIWSQSIATITITAPPGGETUTVET   :   :   :   :   :   :   :   :   :	
QQ	829 GAKNPAASEVIINTOVSATSEATSTSTOVSATSATATASESSTTSQ 874	
ò	683 REPPNHTVTTTEXWSQSYATTTTVTAPPGETDTVLIREPPNHTVTTTEYWSQSYAT 738	CC use by non-prollt instit CC modified and this statement
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2	VSIASETISI LGIQNFTTTGSLEFFALSIEMINTTVVSKNI LLISIEVCSHSKCV	
ολ	739 TTTVTAPPGGTDTVIREPPNPTVT-TTEXWSQSFATTTVTAPPG 783	DR EMBE; 254141; CAA90835.1; DB SCD: 80004936; VMP317W
qo	930 PTVITEVVTSKGTPSNGHSSQTLQTEAVEVTLSSHQTVTMSTEVCSNSICTPTVITSVQ- 988	Hypot
ò	784 CPSTSTGTWASSSGMUTSTIPSESSDHYVNSTTAGIISTGTSSSGMUTTVTGTC A 2	
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g	989 MRSTPFPYLTSSTSSSLASTKKSSLEASSEMSTFSVSTQSLPLAFTCS 1037	Query Match  Bost Local Similarity 24 18:
	844 GMLLSSTTLVTESETTTELICSDGKECSRLSSSSGIVTNPDSNESSIV 891	Matches 243; Conservative
	1038 EKRSTISVSQWSNTVLTNTIMSSSNVISTNEKPSSTISPVNFSSGYSLP 1087	Qy 320 AGSNGIVIVATTRTVTDST
ò	892 TSTVPTASTMSDSLSSTDGISATSSDNVS 920	DD 4 SGSKSTTATTSHSSTTTTSST
QQ	1088 SSSTPSOXSLSTATITINGIKTVYTTWCPLAEKSTVAASSOSSRSVDRFVSSSKPSSSLS 1147	Qy 377 SYLTKTAPIGETATVIVDVPYH
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qq	1148 QTSIQYTLSTATTTISGLKTVYTTWCPLTSKSTLGATTQTSSTAKVRITS-AS 1199	Qy 437 TVSTTEYWSQSFATTTT
ογ	973 NQSGTHDSQSTSTELEIVTTSSTKVLPPVVSSNTDLTSE-PINTREQPTTLSTTS 1026	Db 89 IFSSLSYTSSDISSTSVNDVES
QQ	1200 SATSTSISLSTSTESESSSGYLSKGVCSGTECTQDVPTQSSSPASTLAYSPSVSTS 1255	QY 492 APPGGTDSVI
οy	1027 NSITEDITISQPIGDNGDNISSINPVPTVATSTLASASEEDNKSGSHESASTSLKPSMGE 1086	Db 147 SSPQTSSSNGGGSSSEPLGKSS
đ	1256 SSSSFSTTTASTLTSTHTSVPLLPSSSSISASSPSSTSLLSTSLPSPAFT 1305	Qy 538 IREPPNPTVTTTEYWSQSYA
ογ	1087 NSGLTTSTELEATTTSPTEAPSPAVSSGTDVTTEPTDTREQPTTLSTTSKTNSEL 1141	Db 207TSVGTTSDASKEVFSS
qq		Qy 596 TTVTAPPGGTDTVIIREPPNHT
ò	1142TGTS 1169	:

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-----GAVASASND--QSHSTSVTNS----NSIVS 1210
                                                                                        SETYKSSATISACSGEGCQASATSELNSQYVTMTSVIT 1482
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EMBL/GenBank/DDBJ databases.
ER/THR RICH DOMAIN AND REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTVTAPPGGTDSVIIREPPNHTVTTTEYWSQSYATT 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                              aaker's yeast).
.a; Saccharomycotina; Saccharomycetes;
omycetaceae; Saccharomyces.
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Pred. No. 8.8e-16;
93; Mismatches 379; Indels 195;
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annotation update)
ein in PRE5-FET4 intergenic region.
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MW; 0153EBCA24FE5427 CRC64;
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Query Match
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Matches 313
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                                                                                                                                                                                                                                                                                                                                                                                                                        ASASEEDNKSGSHESASTSLKPSMGENS--GLTTSTEIEATTTS---PTEAPSPAVSSGT 1115
                                                                                                                                                                                                                                                                                                  LSSSVTSLFQLSSIPSVSESESKVTFTSNGDNQSGTHDSQSTSTEIE-IVTTSSTKVLPP 1000
                                                                                                                                                                                                                                                                                                                                                          VVSSNTDLTSEPTNTREQPTTLSTTSNSITEDITTSQPTGDNGDNTSSTNPVPTVATSTL 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVTTEP-----TDTREQPTTLSTTSKTNSELVATTQATNENGGKSPSTDLTSSLTTGTSA 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1171 -----STSANSELVT----SGSVTGGA-----VASASNDQSHSTSVTNSNS 1207
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 TTEYWSQSYATTTTITAPPGETDTVLIREPPNHTVTTTEYWSQSYATTTTVTAPPGETDT 715
                                                          VLIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVIIREPPNPTVTTTEYWSQSFATT 775
                                                                                                                    TTVTAPPGGTDTVIIYESMSSSKISTSSNDITSIIPSFSRPHYVNSTTSDLSTFESSSMN 835
                                                                                                                                                                             TPTSISSDGMLLSSTTLVTESETTTEL - ICSDGKECSRLSSSSGIVTNPDSN - - ESSIV 891
                                                                                   343 VYSSEAPSSTSSSVSEISTTSSSVSSEAPLATSSVVSSEAPSSTSSSVSSEAPSSTSS
                                                                                                                                                                                                                                      TSTVPTASTMSDSLSSTDGLSATS----SDNVSKSGVSVTTETSVTT----IQTTPNP
                                                                                                                                                                                                                                                                                                                            LPSVWSDITS ---- SEASS --- ISSNLASSSAPSDNNSTIASASLIVIKTKNSVVSS
                                                                                                                                                                                                                                                                                                                                                                                       617 IVSSIT--SSETTN----ESNLATSSTSLLSNKATARSLSTS--NATSASNVPTGTFSSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               728 -- TSAPFINNSTSARPSPSTASFITESTSSISSVPLASGDVTSSLAAHNLTTFSAPSTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        786 AOLVSKSTISSSILVTPRIDRSGNSSTASRIATSLPNKTTFVSSLSSTSAHARNIFNSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Loughis Fungi: Ascomycota: Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
MCBL_maxID-4932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1208 IVSNTPQTTLSQQVTSSSPSTNTFIASTYDGSGSIIQHSTWLYGLITLLS 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LATAKQIETLTSTVNCSNPTPNYNITKTV----IVSRETTAIGTVTSCS 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical 122.2 kba protein in SIR1 3'region precursor:
YRR102W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaillon L., Dujon B.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: CELL WALL (BY SIMILARITY).
---- PTM: EXTENSIVELY O-GLYCOSYLATED (BY SIMILARITY).
---- SIMILARITY: STRONG, TO YEAST PROTEIN FLOI.
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P36170;
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K82_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 LSSKTEKRENDDCDQGAAYWSS-DLFGFYTTPTNVTVEMTG-----YFLPPKTGTYT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 FNDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FG------FATVDDSAIL----SV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 NGDVAIDCSNIH---IGIT----KGLNDWN--YPVSSESFSYTKTCTSNGIQIKYQN-VP 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 AGYRPFIDAYISATDVNQ----YTLAYTND------YTCAGSRLQSKPFTL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 -WSSSE------VCTECTETESTSYVTPYVTSSSWSSSEVCTECTETESTSTP 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427 VVVQVPLPNPTVSTTEYWSQSFATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFAT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STPYV-----TSSSWSSSEVCTECTE----TESTSYVTPYVSSSTAAANYTSSFSS 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTVTAPPGGTDSVIIREPPNPTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTV 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 WSLDGTSANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGE-----EFTT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 EKLGSVSGQTKLSIDYSIPCNGASDTCACSDD---DATEYSASQVVPVKRGVKLCSDNTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 TLLFLYLSIASAKTIT------GVFDSFNSLTWSNAANYAFKGPGYPTWNAVLG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 WGTLPVSVVLPDGTEVNDDFEGYVFSFDDNATQAHCSVPNPAEHARTCVSSATSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 YVGVTTSYLTKT-APIGETATVIVDVPYHTTTTVTSEWTGTITTTT---TRTNPTDSIDT
                                                                                                                                                                                                                                                                                                                         LINKED (GLCNAC...) (POTENTIAL)
-LINKED (GLCNAC...) (POTENTIAL)
-140C6DFB3569C669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 YVTSSSSSSSEVCTECTETESTSYVTPYVSSSTAAANYTSSFSSSSEVCTECTETESTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 308;
                                                                                                                                 Glycoprotein; Repeat; Cell wall; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.7%; Score 501; DB 1; Length 1169; 23.1%; Pred. No. 6.9e-15;
                                                                                                                                                                                 HYPOTHETICAL PROTEIN YKR102W.
                                                                                                                                                                                                   SER/THR-RICH.

N-LINKED GECUNAC.

N-LINKED GECUNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 208; Mismatches
send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       879 879
1092 1092
1099 1099
1169 AA; 122164 M
                                                EMBL, Z28327; CAA82182.1; -. PIR; S38181; S38181.
SGD; S0001810; YKR102W.
                                                                                                                           Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LASASEEDNKSGSHESASTSLKPSMGENSGLTTSTEIEATTTSPTEAP---SPAVSSGTD 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1117 VTTEPTDTREQPTT-LSTTSKTNSEL-----VATTQATNENGGKSPSTDLTSSLT-T 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1167 GTSASTSANSELVTSGSVTGGAVASASNDQSHSTSVTNSNSI-VSNTPQTTLSQQVTSSS 1225
                                                                                                                                                                                                                                                                                                                                                                                                         955 IPSVSESESKVTFTSNGDNQSGTHDSQSTSTELEIVTTSSTKVLPPVVSSNTD----- 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTTVSKLESE-------EKTTLITVTSCESGVCSETASPAIVSTATATVND 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1028 VVTVYSTWSPQATNKLAVSDIENSASKASFVSEAAETKSISRNNNFVPTSGTTSIETHT 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSYVTPYVSSTAAAANYTSSFSSEVCTECTETES-----TSTSTPYATSSTGT 612
                                                                                                                                                                                                                                                                                        SASSEQIFHSSIVSSNGQALTSFSSTKVSSSESSESHRTSPTT-----SSESGIKSSG 825
                                                                                                                                                                                                                                                                                                                                                             924
                                                                                                                                                            SSNKGSVKSYVTSSIHSITP------MYPSNQTVTSSSVVSTPITSESSESSASVTIL 713
                                                                                                                                                                                                                              P-STITSEFKPSTMKTKVVSISSSPTNLITSYDTTSKDSTVGSSTSSVSLISSISLPSSY 772
                                                                                                                                                                                                                                                                  894
                                                                                                                                                                                                                                                                                                                                        VPTASTMSDSLSSTDGISATSSDNVSKSGVSVTTETSVTTIQTTPNPLSSSVTSLTQLSS 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             925 RMTSETPSTNEQTTLITVSSCESNSCSNTVSSAVVSTATTTINGITTEYTTWCPLSATE- 983
                                                    667 ITIIIAPPGETDIVLIREPPNHIVITIEYWSQSYAITITVTAPPGETDIVLIREPPNHIV
                                                                               ATSFTASTSNTMTSLVQ-----TDTTVSFSLSSTVSEHTNAP-----TSSVESNASTFI
                                                                                                                        TTTEYWSQSYATTTTVTAPPGGTDTVIIREPPNPTVT----TTEYWSQSFATTTTVTAP
                                                                                                                                                                                               PGGTDTVIIYESMSSKISTSSNDITSIIPSF---SRPHYVNSTISDLSTFESSSMNTPT
                                                                                                                                                                                                                                                                    SISSD----GMLLSSTTLVTESETTTELICSDGKECSRLSSSSGIVTNPDSNESSIVTST
                                                                                                                                                                                                                                                                                                                                                                                                                                          ----STNSSKETMSSE-NSASVMPSSSATSPKTGKVTSDET-----SGFSRDRTTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ictalurid herpesvirus 1 (Channel catfish virus) (CCV). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; unclassified Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Channel catfish virus: a new type of herpesvirus."; virology 186:9-14(1992).
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01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical gene 50 protein.
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MEDLINE-92087490; Pubmed-1727613;
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Q00130;
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 TCAGSRLQSKPFTLRWT--GYKNS--DAGSNGIVIVATTRTVTDST------TAV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPVPREPS-----SLPRTTPSLAHTTISKMISLGTRPRPTIPGVPTTIPNTDAP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              579 TVLIREPPNHTVTTTEYWSQSYATTTTVTAPPGETDTVLIREPPNHTVTTTEYWSQSYAT 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TCLGMSLLASNLALVGVVRSYTNETPTPGPETELITTTVARMTDPTAKPSDFPGDAVTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 TTLPFNPSVDKTKTIEILQPIPTTTTTSYVGVTTSYLTKTAP---IGETATVI--VDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 ----YHTTTVTSEWTGTITTTTTTTNPTDSIDTVVVQVPLPNPTVSTTEYWSQSFATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIVIAPPGGIDTVIIREPPNHTVITIEYWSQSFATITIVIAPPGGIDSVIIREPPNPTVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      632 TTVTGPPSGTDTVIIREPPNPT-----VTTTEYWSQSYAT-----TTTTITAPPGETD
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24.3%; Pred. No. 1.4e:
tive 71; Mismatches
     is not removed
modified and this statement is not removentities requires a license agreement (( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                             64174 MW;
                                                                                     EMBL; M75136; AAA88153.1; -. PIR; F36791; F36791. Hypothetical protein; Repeat REPEAT 143 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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670 AA;
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That Local Sim.
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	589 KPAGANCIVITITAKPAGANGIVITITAKPAGANGIVITITAK 631	589	q
	1095 -EIEATTTSPTEAPSPAVSSGTDVTTEPTDTREQPTTLSTTSK 1136	1095	οy
588	AKPTGANGTVTTT-AKPTGATGTVTTTTAKPTGANGTVTTTTAKPAGANGTVTTTA	532	đ
1094	1036 SQPTGDNGDNTSSTNPVPTVATSTLASASEEDNKSGSHESASTSLKPSMGENSGLTTST-	1036	
531	•	491	q
1035	978 HDSQSTSTEIEIVTTSSTKVLPPVVSSNTDLTSEPTNTREQPTTLSTTSNSITEDITT 1035	978	ογ
490	445 TANVTKPTGATDTVVTTATVKPTGATGTVTTTAKPTGANDTANVT 490	445	QQ
677	918 NVSKSGVSVTTETSVTIQTTPNPLSSSVTSLTQLSSIPSVSESESKVTFTSNGDNQSGT 977	918	ογ
444	TTPAKPAGANGTVVTTTPAMPAGANDTVVTTAPATPAGAND 444	404	qo
917	TTELICSDGKECSRLSSSSGIVTNPDSNESSIVTSTVPTASTMSDSLSST-DGISATSSD	859	δ
403	T 403	403	qq
828	799 ISTSSNDITSIIPSFSRPHYVNSTTSDLSTFESSSMNTPTSISSDGMLLSSTTLVTESET	799	Qy
402	TTTP	358	qq
798	TTTVTAPPGGTDTVIIREPPNPTVTTTEXWSQSFAT	739	ογ

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        Ogvtk8 drosophila
OgcOy2 schizosacch
O76602 caenorhabdi
P91365 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-AUCCIOS61;
Leng P., Lee P.R., Wishart J.A., Wu H., Brown A.J.P.;
"Sequence of the hypha-specific, agglutinin-like cell surface protein, from Candida albicans";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP051313; AAD02580.1;
SEQUENCE 1047 AA; 111944 MW; C2327659Aa911F2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
62.8%; Score 4078.5; DB 3; Length 1047;
Best Local Similarity 65.0%; Pred. No. 2.7e-180;
Matches 822; Conservative 100; Mismatches 120; Indels 223; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ANPGDIFTLIMMPCVFKYTTSOTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLQQFTLLFLYLSIASAKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          093865 PRELIMINARY: PRT; 1047 AA.
093865; 00.4847-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALSE
Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
NCBL_TRANDES; mitosporic Saccharomycetales; Candida.
      Q9VTK8
Q9C0Y2
O76602
P91365
Q99QY4
Q99552
Q939NS
                                                                                          Q96WX6
Q9AE52
Q9USQ3
O14651
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                                                                                                                                                                                                                                                                                              720
                                                -----TAPPGETDTVLIREPPNHTVTTTEYWSQSYATTTVTA 744
                                                        PPGGTDTVIIREPPNPTVTTTEYWSQSFATTTTVTAPPGGTDTVIIYE----SMSSSKIS 800
                                                                                      TSSNDITSIIPS-----SPRPHYVNSTTSDLSTFESSSMNTPTSIS-----SDGML 846
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O1-NOV-1999 (TEMBLEEL 12, L.
O1-DEC-2001 (TEMBLEEL 19, L.
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68 TLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKSSIKAFGT 127
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                                                                                                                                                                                                                                                                                                   Query Match
43.0%; Score 2791.5; DB 3; Length 1443;
Best Local Similarity 44.2%; Pred. No. 6.7e-121;
Matches 642; Conservative 202; Mismatches 387; Indels 223; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  VTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAYLYAS 187
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Candida albicans (Yeast).
Makaryota; Fungl; Ascomycota; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_maxID-5476;
                                                                                                 ETRAIN-161;

WDELINE-203177; PubMed-10861907;

HOYOF L.L., Hecht J.E.;

Yeast 16:87-855(2000).

EMBL; AD075293; AAD042033.1; --

InterPoo, IPR003015; HELIX_LOOP HELIX; UNKNOWN I.

SEQUENCE 1443 AA; 151476 MW; DCBD693F4C435809 CRC64;
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us-09-715-876-8.rspt

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1055 VATSTLASASEEDNKSGSHESASTSLKPSMGENS-----GLTTSTEIEATTTSPTEA- 1106
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                                                                                                                                                                                                                                                                                     1012 PINTREOPTILSTISNSITED----ITTSOP-----TGDNG------DNTSSTNPVPT 1054
                                                                                                                                                                             :::: : | || || || || 844 SSSDDFPHTIAGESDSLSISFITSTVEISSDSVSLTSDPASSFDSSSSLNSDSSSSPSSD 903
                                                                                                        803 SNDI-----TSIIPSES-----RPHYVNSTTSDLSTFESSSMNTPTSISSDGM 845
---PNPTV 762
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                          SHLVQSVSNSISTSQELSSSSSEESSTF----ATDALVSSDASSILSSDTSSYYPSSTI
                                                     763 TITIEYW-----SQSFATIT-----TVTAPPGGT-DTVIIYESMSSSKISTS
                                                                                                                                                            846 LLSSTTLVTESETTTELICSDGKE---CSRLSSSSGIVTN-PDSNESSIVTSTVPTASTM
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01-NOV-1999 (TIEMBLRel. 12, Last sequence update)
01-NOV-1999 (TIEMBLRel. 12, Last sequence update)
01-DEC-2001 (TIEMBLREL. 19, Last annotation update)
AGGLOTINIA LIKE PROTEIN.
ALSS
Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetels;
Saccharomyceteles; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
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MEDIAL THE LOOK N.A.
STRAIN-1161;
MEDIAL THE LOOK STRAIN-1161;
HOYER L.L., Hecht J.E.;
HOYER L.E., Hecht J.E.;
HEARD Spene of Candida albicans and analysis of the Als5p I terminal domain.;
Fast 18.49-60(2001).
EMBL; AC68866, AAD32849.1; -.
SEQUENCE 1270 AA; 133337 WW; DRESFAS853F6D5C5 CRC64;
 715 TVLIREPPNHTVTTTEXWSQSYATTTTVTAPPGGTDTVIIREP-
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                                                                                                                                                                                         301 SRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQ 360
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                                                                                                                               SIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDP 180
                                                                                                                                              SAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLND 240
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                                                                                     61 ANPGDIFILIMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKS 120
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                                                       1 MLQQFTLLFLYLSIASAKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTS 60
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DB 3; Length 1270;
                     Indels
41.2%; Score 2673.5; DB 3; Similarity 45.9%; Pred. No. 1.6e-115; 9; Conservative 187; Mismatches 340;
  Query Match
Best Local Simmatches 629;
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                                                                                                                                                                                                                                                                              YWSQSFATTTTVTGPPSGTDTVIIREPPNPTVTTTEYWSQSYATTTTTAPPPGETDTVLI 682
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   GSRLQSKPFTLRWT-GYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEI 358
                 : | :|||:|| | DIDLVDIVIVKIPYPNPIIITTQFWSGKYLTTETHKEPPLGTDSVIIKEPHNPTVTTE
                                                                                                                                                                         TAVSDI--SDLYTTSEEVSTSDSNSGMSSPI-PSSEQRS-----SIPIMSSSDESSESR
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                                                                                                                                                         YWSQSFATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFATTTTVTAPPGGTDSVII
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----EQPTTLSTTS 1026
                                                                                                                             1045 -- TLGENSFSNVASTPLNTATSLRSTSSSSNHATE---SSGTVKSEASVEALPSPPTSTD 1099
              SSHKSTASIKESSIQKTGVTLSSSYLSTKISSTSDITIELITTELTTIEDNEPNTFTSTP 996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 SANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 211; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSITEDITTSQPTGDNG-----DNTSSTNPVPTVATSTLASASEEDNKSGSHESASTSL
                                                                   1081 KPSMGENS-----GLTTSTEIEATTTSPTEAPSPAVSSGT------DVTTEPTDT-
                                                                                                                                                       1125 ------REOPTILSTISKIN----SELVATIQAIN---ENGGKSPSIDLISSLITGI
                                                                                                                                                                          1100 NRLSYSTEEAEGITYANSGSTNNLITESQVAAPTDSTSVLIENLVVTSTFDDNSSAAVDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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39.7%; Score 2576.5; DB 3; Length 2297;
Best Local Smilarity 41.3%; Pred No. 8.7e-111;
Matches 595; Conservative 220; Mismatches 416; Indels 211;
                                                                                                                                                                                                                                                             1209 VSNTPQTTLSQQVTSSSPSTNTFIASTYDGSGSIIQHSTWLYGLITLLSLF 1259
                                                                                                                                                                                                                                                                              1220 ASNSQPTTLIQQVATS--SYNQPLITTYAGSSSATKHPSWLLKFISVALFF 1268
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MEDLINE-2013117; PubMed-10861907;
MEDLINE-2013117; PubMed-10861907;
"The ALS6 and ALS7 genes of Candida albicans.";
"The ALS6 and ALS7 genes of Candida albicans.";
EASEL; AS201684; AAP1980681; --
SEQUENCE 2297 AA; 244723 WW; 59B020C63027F651 CRC64;
GTHDSQSTSTEIEIVTTS---STKVLPPVVSSNTDLTSEPTNTR---
                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-BC-2001 (TrEMBLrel. 19, Last annotation update)
AGGLUTININ-LIKE PROTEIN ALS/P.
                                                                                                                                                                                                                                                                                                                                                       PRT; 2297 AA
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1368 PIPSSEQRSSIPVMSSSDESSESRESSSGTILSEENSDSIPT--TFSTRYLSPSGMSSRH 1425
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SEQUENCE FROM N.A.
SETARIA-1161;
MEDLINE-98440424; PubMed-9765564;
HOYEr L.L., Payne T.L., Hecht J.E.;
"Identification of Candida albicans ALS2 and ALS4 and localization in the fungal cell surface.";
J. Bacteriol. 180:5334-5343(1998).
J. Bacteriol. 180:5334-5343(1998).
NON_FER 468
SEQUENCE 468 AA: 50143 MW; 2E38E36D7FEAD192 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans (Yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotes; Saccharomycotales; Mitosporic Saccharomycotales; Candida.
NGBI_TaxID=5476;
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30.6%; Score 1986.5; DB 3; Length 468;
Best Local Similarity 80.0%; Pred. No. 2.44-64;
Matches 375; Conservative 33; Mismatches 60; Indels 1;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
AGGLUTININ-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                            468 AA
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RESULT Q9URP8

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                                                                                                                                                                                                                                                                                                STRAIN-1161;
STRAIN-1161;
STRAIN-1161;
MEDLINE-98440444; PubMed-9765564;
Hoyer L. L., Payne T. L., Hecht J.E.;
"Identification of Candida albicans ALS2 and ALS4 and localization of als proteins to the fungal cell surface.";
J. Bacteriol. 180:5334-5343(1998).
EMBL; AF024586; AAC64241.1;
NON_TER 469 46997 MM; 88BC96D79142C8DB CRC64;
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Kakaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
NCBL_TaxID=5476,
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Candida albicans (Yeast).
Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Candida.
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28.1%; Score 1823; DB 3; Length 469;
Best Local Similarity 72.1%; Pred. No. 8e-77;
Matches 338; Conservative 49; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 TDSIDTVVVQVPLPNPTVSTTEYWSQSFATTTTVTAPPGGTDTVIIREP 469
Q9URP8 PRELIMINARY; PRT; 469 AA.
Q9URP8; 01-MXY-2000 (TrEMBLrel. 13, Created)
01-MXY-2000 (TrEMBLrel. 13, Last sequence update)
01-MXY-2000 (TrEMBLrel. 13, Last annotation update)
AGGLUTININ-LIKE PROTEIN (FRAGMENT).
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18.3%; Score 1191; DB 3; 64.8%; Pred. No. 7.1e-48; Live 51; Mismatches 66;
                                            22.6%; Score 1471; DB 3;
81.0%; Pred. No. 9.1e-61;
iive 31; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 PIPTTITTSYVGVTTSYLTKTAPIGETATVIVDVP 396
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Matches 219; Conservative
                                                                                     Conservative
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                                                                Best Local Similarity
Matches 272; Conserv
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SEQUENCE
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Q9HF72
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"Evidence suggesting the presence of an ALS gene family in Candida dublintensis and candida tropicalis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF202529; AAG35623.2;
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TaxID-42374;
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                                                                                                                                                                                                                                                              Ouery Match 27.4%; Score 1780.5; DB 3; Length 468; Best Local Similarity 70.1%; Pred, No. 7.2-75; Matches 329; Conservative 62; Mismatches 77; Indels 1; Matches 329; Conservative 62; Mismatches 77; Indels 1; Matches 789; Conservative 62; Mismatches 77; Indels 1; Matches 789; Conservative 62; Mismatches 77; Indels 1; Matches 789; Mismatches 789; Mis
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                                                                             Hoyer L.L., Hecht J.E., Mirus K.A.;
The ALS9 gene of Candida albicans.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR22999; AAK00764.1;
NON TER
SEQUENCE 468 AA; 50127 MW; B291D3EB15FB96DE CRC64;
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336 AA; 35593 MW; E513E6EA9E8E9EC7 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 17, Last annotation update)
AGGLUTININ-LIKE PROTEIN ALSD2P (FRAGMENT).
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                                         SEQUENCE FROM N.A.
NCBI_TaxID=5476;
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Hoyer L.L., Hecht J.E., En J., Kapteyn J.C., Klis F.M.;
Evidence suggesting the presence of an ALS gene family in Candida dubliniensis and Candida tropicalis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
BNBL, AF201685; AAG35603.1; -.
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Length 336;
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                                               Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2013W-2001 (TrEMBLrel. 17, Last annotation update)
AGGLUTININ-LIKE PROTEIN ALSDIP (FRAGMRNT).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Ol-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AGGLUTIXIN-LIKE PROTEIN 7 (FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida tropicalis (Yeast).
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 46.08
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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421 DDIDLVDTVIVKI 433
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Q9HF71
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                 61 QTKALGTVTLPLSFNIGGSGSDVDITSSQCFKEGTNTVTFNDGDTTFSTTANFQRSDVNA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 AGSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ANPGDIFILNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 SAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLND 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NDRILLSRILPSLAKSVTIFIPPRCASGYSSGTMGFSTAGTDAIIDCSTVHAGISNGLND 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIGURE 1. Hecht J.E., En J., Kapteyn J.C., Klis F.M.;
HOyer L.L., Hecht J.E., En J., Kapteyn J.C., Klis F.M.;
Hoyer L.L., Hecht J.E., En J., Kapteyn J.C., Klis F.M.;
Evidence suggesting the presence of an ALS gene family in Candida dublinienesis and candida tropicalis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF102530; AG35624.2;
NOM_TER 1 331
NOM_TER 331
NOM_TER 331
SEQUENCE 331 AA; 35297 MW; 469AB72F9CE029BF CRC64;
WNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQ--YTLAYTNDYTC
                                                                                                                                                                                                                                                                                                                                                              Candida dubliniensis (Yeast).
Bukaryota; Kungi, Ascomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=42374;
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                                                                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
AGGLUTININ-LIKE PROTEIN ALSD3P (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
18.1%; Score 1176; DB 3;
Best Local Similarity 64.3%; Pred. No. 3.4e-47;
Matches 214; Conservative 44; Mismatches 73;
                                                                                                                            433 AA
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                                                                                                                                                                                                                                               PRELIMINARY;
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Q9Y8F1
ID Q9Y8F1
AC Q9Y8F1
DT 01-NOV
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60 SANPGDIFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALS7.
Candida albicans (Yeast).
Cardida albicans (Yeast).
Sackaryota; Fungi; Ascomycota; Saccharomycotales; Saccharomycetales; Mitosporic Saccharomycetales; Candida.
NCBL_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TaxID=5482;
                                                                                                                                                                                                                                                                                                                                                               15.4%; Score 999.5; DB 3; Length 433; 46.0%; Pred. No. 6e-39; Live 76; Mismatches 155; Indels 3
                                                                                                                                                                                                                                                                                                  433 AA; 48037 MW; 1F30CFD99C2EC445 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
AGGLUTININ-LIKE PROTEIN 1 (FRAGMENT).
                                                                                                                                               STRAIN-1161;
MEDLINE-20321177; PubMed-10861907;
MEDLINE-20321177; PubMed-10861907;
"The ALSG and ALS7 genes of Candida albicans.";
Yeast 16:847-855(2000).
EMBE: AF075294; AAAA2034.1; -
NON_TER 433 A3; 48037 WW; 1F30CFD99C2EC445
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VOPTIGATGTAGTETQVITGTETQATTATETQATTATEVQTTTGATGTAGTE----TQVT 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               038 PTGDNGDNTSSTNPV---PTV-ATST-----LASASEEDNKSGSHESASTSLKPSMGEN 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         862 LICSDGKECSRLSSSSGIVTNPDSNESSIVTSTVPTAS---TMSDSLSSTDGISATSSDN 918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   810 IPSFSRPHYVNSTISDLSTFESSSMNTPTS---ISSDGMLLSSTTLVTESETT----TE 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 VETPYPTTVTTTTVGYPGSVTTTLTGAPSNGTVIDTVEIPTTNYGYTTITTGYTGSTT 119
                                                                                                                                                                                                                                                                                                                                                                                                                   654 ---VTTTEYWSQSYATTTITAPPGE---TDTVLIREPPNHT-----VTTTEYWSQSYA 701
                                                   AVITLPFNPSVDKTKTIEILQPIPTTTTTTSYVGVTTSYLTKTAPIGETATVI--VDVPY 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      904 TQATTATETQATTATEVQTTTGATGTETQATTATEVQPTTGATGTAGTETQVTTATE
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                                                                     HTT---TTVTSEWTGTITTTT-----RTNPTDSIDTVVVQVPLPNPTVSTTEYWSQSF
                                                                                                                                                                                           501 IIREPPNPTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVTTTEY-----W
                                                                                                                                                                                                                                                        553 SQSYATTTVT--APPGGIDSVIIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTVII
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TATEV-----QPTTAVTETSSSGYYTTIVSST 1046
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                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                         Hoyer L.L., Hecht J.E., En J., Kapteyn J.C., Klis F.W.;
"Evidence suggesting the presence of an ALS gene family in Candida dubliniens!s and Candida tropicalis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF201686; AAG35604.1; -...
NON_TER 1 1 1
NON_TER 353
SEQUENCE 353 AA; 37272 MW; 4268154D5615DE08 CRC64;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ALS91677; CAS39226.1; -.
Hypothetical protein.
NON_TER 1195 1195
                                                                                                                                                             Length 353
                                                                                                                                                                                           Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
SPCPB16A4.07C.
Schlzosaccharomyces pombe (Fission yeast).
Schlzosaccharomycetales; Schlzosaccharomycetes; Schlzosaccharomycetes;
                                                                                                                                                             15.1%; Score 981; DB 3; L
54.9%; Pred. No. 3.5e-38;
:1ve 50; Mismatches 100;
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                                                                                                                                                                           Best Local Similarity 54.99
Matches 185; Conservative
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NCBI_TaxID=4896;
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SEQUENCE FROM N.A.
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Best Local Similarity
Matches 319; Conserv
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SEQUENCE
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 IVTAPPGGTDSVIIREPPNPTVTTTEYWSQSFATTTTVTAPPGGTDSVIIREPPNPTVTT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         549 TEYWSQSYATTTTVTAPPGGTDSVIIREPPNHTVTTTEYWSQSYATTTTVTAPPGGTDTV 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoyer L.L., Kapteyn J.C., Hecht J.E., En J., Klis F.M.;

"Exidence Suggesting the Presence of an ALS Gene Family in Candida dubliniensis and Candida tropicalis.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AF189016; AAG17111.1;

NON_TER 226

SEQUENCE 226 AA; 24802 MW; 2AA36A42E44CB460 CRC64;
                                                                                                                                                                                                  ALS5.

Acidida albicans (Yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

NCBL_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.7%; Score 824; DB 3; Length 226; Best Local Similarity 70.1%; Pred. No. 3.7e-31; Matches 155; Conservative 28; Mismatches 38; Indels
Q9HG16
AC 09HG16 PRELIMINARY; PRT: 226 AA.
AC 09HG16 PRELIMINARY; PRT: 226 AA.
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
CG NACOLITININ-LIKE PROTEIN (FRAGMENT).
CG NACOLITININ-LIKE PROTEIN (FRAGMENT).
CG Saccharomycetales; mitosporic Saccharomycetales; Candid
NCB1_TAXID=5476;
RN 11)
RP SEQUENCE FROM N.A.
RC STRAIN=1177;
RA HOYEL L.L. Kapteyn J.C., Hecht J.E., En J., Klis F.M.;
RT Mubliniensis and Candida tropicalis.';
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
DR EMBL, AF189016; AAG17111.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 226
226 AA; 24802 MW; 2AA36A42E44CB460 CRC64;
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Search completed: October 3, 2002, 15:37:25 time: 306 sec

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October 3, 2002, 16:25:37; Search time 31.64 Seconds (without alignments) 1460.389 Million cell updates/sec
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2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAl981_DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAl981_DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAl981_DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAl981_DAT:*
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2190
1 AKTITGVFDSFNSLTWSNAA......TTTTRTNPTDSIDTVVVQVP 416
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Alpha-aqqlutinin o	Yeast 4.7 kB agglu	Cryptosporidium pa	Cryptosporidium pa	Portion of Cryptos	Peptide #2788 enco	Peptide #2813 enco	Protein #2748 enco	Human brain expres	Human bone marrow	Peptide #2749 enco
SUMMARIES			ΩI	AAR47575	AAR60562	AAB11726	AAW48299	AAB11727	ABB30137		ABB20749	AAM56138	AAM6851.1	AAM16315
			80	15	15	71	19	21	22	22	22	22	22	22
			e Match Length DB I	650	1537	1837	1721	1721	689	688	688	689	689	688
	æ	Query	Match	14.1	8.1	8.0	8.0	8.0	7.1	7.1	7.1	7.1	7.1	7.1
			Score	308.5	177	175.5	175	175	156	156	156	156	156	156
		Result	S S	1	7	m	7	ស	9	7	80	6	10	11

Toschka H, Verrips CT;

Klis FM, Schreuder MP,

WPI; 1994-035071/04. N-PSDB; AAQ54012.

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23	S		æ	22	983	ide #2
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56	S		В	22	AAM55821	brain
27	S		œ	22	319	ne n
28	S		B	22	501	de #244
29	5		B	22	851	#255
30	S		В	22	374	eptide #2431
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35	46.		53	21	94	Human ORFX ORF709
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39	4	•	96	12	920	protease
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42	4	•	96	13	355	t protease
. 43	4		96	13	920	protease
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45	4	•	97	13	94	<b>388</b> 6
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Immobilisation; enzyme; cell wall; alpha agglutinin; ACA 1; FLO 1; Major cell wall protein; glycosyl-phosphatidyl-inositol; anchoring protein; alpha factor; alpha-agglutinin; invertase; inulinase; alpha-amylase; Saccharomyces cerevisiae; enzymatic process; fermentation; blodegradation; catalysis.
                                                                                   Alpha-agglutinin of Saccharomyces cerevisiae.
AAR47575
ID AAR47575 standard; Protein; 650 AA.
XX
                                                                                                                                                                                                                                      93WO-EP01763
                                                                                                                                                                                                                                                         92EP-0202080.
                                                             19-JUL-1994 (first entry)
                                                                                                                                                                       Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                          (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                     07-JUL-1993;
                                                                                                                                                                                                                                                         08-JUL-1992;
14-DEC-1992;
                                                                                                                                                                                           WO9401567-A.
                                                                                                                                                                                                                 20-JAN-1994
                                        AAR47575;
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20;
                                                                                                                                                    The alpha-aggluthin is used in a method to immobilise enzymes to a microbial cell wall. The coding sequence is used in the production of a recombinant polyvuclectide which comprises a structural gene encoding a protein with catalytic activity and at least part of a gene encoding at least the C-terminus of a protein capable of from confing in a enkaryotic or protein capable of ragent or protein is selected from alpha aggluthin, AGA 1, FLO 1, major cell wall protein of lower eukaryotes or a proteinase of lactic acid bacteria. The recombinant polynucleotide preferably also comprises a sequence encoding a signal peptide to ensure secretion of the expressed product. The signal peptide to ensure protein, alpha factor, alpha aggluthin, invertuse or inulinase, alpha-maylase of Bactilus or proteinases of lactic acid bacteria.

The host microorganism can be used for performing enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 slnfsdggssyeyelenakffksgpmlvklgngmsdv---vnf----dpaaftenvfhs 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 RVMPSLNKVTTLFVAPQCENGYTSG---TMGFSSSNGDVAIDCSNIHIGITKGLNDWNYP 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 PIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAY---LYAS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 qsyndtnadvtcfgsnlwitldeklydgemlwvnalqslpanvntidhalefgytcldti 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 AGSRLQSKPFTLR----WTGYKNSDAGSNGIVIVATTRTVTD-----STTAVTTLPFNP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 SVDKTKTIEILQPIPTTTTTTSYVGVTTSYLTKTAPIGETATVIVDVPYHTT----- 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 etgnrttsevishvvttstklsptattsltiaqtslystdsnitvgtdihttsevisdve 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.1%; Score 308.5; DB 15; Length 650; 25.8%; Pred. No. 2.7e-16; Live 79; Mismatches 190; Indels 65; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 ninditfsnleitpltan---kqpd-qgwtatfdfsladasslregdeftlsmphvyrik 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 SFNSLTWSN-----AANYAFKGPGYPTWNAVLGWSL-DGTSANPGDTFTLNMPCVFK-- 60
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                         of
                         Immobilisation of enzymes to microbial cell wall - by prodn. fusion protein of enzyme linked to anchoring protein
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                                                                                                          Example 1; Page 32-39; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR60562 standard; Protein; 1537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.84
Matches 116; Conservative
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163 ailsvggatafnccaqqqppltstnftldgikpwggslppniegtvymyagyyypm--- 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The agglutination gene is called FLO1. Saccharomyces cerevisiae includes an agglutination gene of 4.7 kb (FLO1b) and an agglutination gene of 2.6 kb (FLO1s). FLO1L is the inteat FLO1 gene on chromosome I, and FLO1s is the FLO1L gene with a portion of the ORF deleted in frame. FLO1L imparts a relatively strong agglutinative property to the host yeast into which it is introduced, while FLO1s imparts a weaker agglutinative property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 nwgckgmgacsnsgglaywstdlfgfyttptnv-tlemtgyflppgtgsytfkfatvdds 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 rtpttastiitttepwnstftststelttvtgtngvrtdetii-----virtpttatta 366
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                                                                                                                                                                                                                                                                                                                                                                           New yeast agglutination genes and yeast contg. them - impart agglutination properties to facilitate removal from fermentation media
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1537;
                                                                                                                                                                                                                                                                        Takata Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

8.1%; Score 177; DB 15;
Best Local Similarity 23.0%; Pred. No. 3.5e-05;
Matches 112; Conservative 47; Mismatches 181;
                                                                                                                                                                                                                     PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM
                                                                                                                                                                                                                                                                  Penttila M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 43-48; 75pp; English;
                                                                                                                                                                                                                                                                        Keraenen S, Ogawa M, Onnela M,
Watari J;
                                  Saccharomyces cervisiae ABXL-1D.
                                                                                                                                                                                93JP-0038871.
Yeast; agglutination; FLO1L.
                                                                                                                                           94WO-JP00290
                                                                                                                                                                                                                                      SAPB ) SAPPORO BREWERIES
                                                                                                                                                                                                                                                                                                                            WPI; 1994-294338/36.
N-PSDB; AAQ71390.
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                                                                                                                                              24-FEB-1994;
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                                                                                                         01-SEP-1994.
                                                                    WO9419475-A
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qq
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Cryptosporidium parvum GP900 antigen.
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175..423
/note= "NINC domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW48299 standard; Protein; 1721 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US14104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0700651
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N-PSDB; AAV20700, AAV20701.
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                           1837 AA;
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                            Sequence
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parvum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the GP900 glycoprotein of the protozoan cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion proteins comprising GP900 fragments. The invention also relates to the administration of GP900 or fragments thereof to a host to elicit anticant to antibody production, and to a method of Cryptosporidiosis treatment or prophylaxis comprising administration of anti-GP900 antibodies to an individual. Cryptosporidium parvum GP900 and GP900 fragments are able to competitively inhibit sporozoite or merozoite attachment or invasion, and care also useful for the generation of anti-GP900 antibodies. The additionally inhibit sporozoite or merozoite attachment/invasion and additionally inhibit the binding of GP900 injugands to GP900. GP900 antibodies. The additionally inhibit the binding of GP900 injugands to GP900. GP900 cortens, fragments and antibodies may therefore be used to treat or protosporidioss. Infection with Cryptosporidium is a common cause of diarrhoea in humans and causes life-threatening diarrhoea in munocompromised persons. Cryptosporidiosis can be contracted from contaminated municipal water supplies (e.g., public swimming pools). It is also a cause of disease in animals, resulting in financial losses in addiction of the parasite in the environment. The present sequence represents the GP900 protein of the lowa isolate of Cryptosporidium
                                                                                                                                                                                                                        GP900; Iowa isolate; glycoprotein; antibody; cryptosporidiosis; competitive inhibition; attachment; invasion; ligand binding; sporozoite; merozoite; diarrhoea; protozoacide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900
                                                                                                                                                                                                                                                                                                             Key
Location/Qualifiers
Misc-difference 1785
/note= "Encoded by AAC in AAA61846"
                                                                                                                                                                                                  Cryptosporidium parvum Iowa isolate GP900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Column 51-60; 59pp; English.
                                                                                                             AAB11726 standard; Protein; 1837 AA.
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92US-0891301.
95US-0415751.
96US-0700651.
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N-PSDB; AAA61846, AAA61847.
                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                   Cryptosporidium parvum.
                                  532 -etilv 536
          408 IDTVVV 413
                                                                                                                                                                     28-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-1997;
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14-AUG-1996;
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 TSANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDAL 102
                                                                                                                                                                                       152 SIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAI -- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 ----DCSNIHIGITKGLNDWNYPVSSESFS------YTKTCTSNGIQIKY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 QNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         670 gaihsgygtsadfvtttt------ttgapgg 700
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                                                                         Gaps
                                                                                                                                                                                                                                                                            103 KSSIKAFGTVTLPIAFNVGGTGSSTDL------EDSKCFTAGTNTVTFNDGDKDI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Open reading frame; ORF; antigen; GP900; cryptosporidium; infection; antibody; propphylaxis; treatment; inhibition; retardation; detection; diagnosis; human; 3' region.
Ouery Match 8 0%; Score 175.5; DB 21; Length 1837; Best Local Similarity 2:9%; Pred No. 5.9e-05; Matches 93; Conservative 45; Mismatches 176; Indels 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             753 attttlkpivttttkattttttttvptttt-ttkrdemtttttplp 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 GETATVIVDVPYHTTTTVTSEWTGTITTTTTTTRTNPTDSIDTVVVQVP 416
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16;
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                                                                                                                                                                                                                                                                                                                                                                              43 TSANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDAL 102
                                                                                                                                                                                                                                                                                                                                                                                                         439 igkägriengmaftmipndathvrfrfkvkdvgntisv----rcrkg--agklefpdrs 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 AGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTTITTSYVGVTTSYL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 KSSIKAFGTVTL----PIAFNVGGTGSSTDLEDS--------KCFTAGTNTVTF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 kpttttttttttttttkptttttatttttsetesvikpdewcwlekngeceakgatyvgv 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 GIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSD 303
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                         The sequence is that of the GP900 antigen which may be used in the production of anti-Cryptosporidium antibodies. These can be used for the prophylaxis, treatment, inhibition or retardation of a Cryptosporidium infection in humans or in animals such as calves. They can also be used for the detection and diagnosis of related
to develop products for treatment of Cryptosporidium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 NDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 GDVAI------DCS-----NIHIGI--TKGLNDWNYPVS-SESFS--YTKTCTSN
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                                                                                                                                                                                                                                                                                                    Length 1721;
                                                                                                                                                                                                                                                                                                    8.0%; Score 175; DB 19; Length 172
23.2%; Pred. No. 5.9e-05;
tive 41; Mismatches 180; Indels
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Anti-Cryptosporidium antibody - used detection, diagnosis, prophylaxis or
                                                                     Claim 27; Pages 65-68; 89pp; English.
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Best Local Similarity 23.2%
Matches 96; Conservative
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01-JUN-1993;
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infections.
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The invention relates to the GP900 glycoprotein of the protozoan Cryptosporialum parvum, DNA encoding it, GP900 fragments, and fusion proteins comprising GP900 cragments. The invention also relates to the administration of GP900 or fragments thereof to a host to ellcit anticorportation of GP900 or fragments thereof to a host to ellcit anticorportation of GP900 antibodies to an individual cryptosporialum parvum GP900 and GP900 antibodies to an individual cryptosporialum parvum GP900 and GP900 fragments are able to competitively inhibit sporozoite or merozoite attachment or invasion, and are also useful for the generation of anti-GP900 antibodies. The are also useful for the generation of anti-GP900 antibodies. The are also useful for the pencation of merozoite attachment or invasion, and antibodies also inhibit sporozoite or merozoite attachment or invasion, and additionally inhibit the binding of GP900 ligands to GP900 appending and antibodies may therefore be used to treat or prevent cryptosporialosis. Infection with Cryptosporialum is a common cause of diarrhoea in humans and causes life threatening diarrhoea in munucoompromized persons. Cryptosporialosis can be contracted from conteminated municipal water supplies, (e.g., public swimming pools). It is also a cause of disease in animals, resulting in financial losses in agriculture. GP900 fragments of Cryptosporialum parvum infections and for the exciton of the parasite in the environment. The present sequence represents a portion of the GP900 protein of the NINC isolate of Cryptosporialum parvum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 GIQIKYONVPAGYRPFIDAYISATDVNOYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSD 303
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Column 61-70; 59pp; English.
92US-0891301.
95US-0415751.
96US-0700651.
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N-PSDB; AAA61848, AAA61849.
                                                                                              (REGC ) UNIV CALIFORNIA.
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29-MAY-1992;
03-APR-1995;
14-AUG-1996;
                                                                                                                                               Petersen C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                              Peptide #2788 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
Human; microarray; single exon probe; gene expression; breast;
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                                                                                               ABB30137 standard; Peptide; 688
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30-UN-2000; 2000US-0608408.
03-AUG-2000; 2000US-023366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023459.
04-CCT-2000; 2000GB-0024683.
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                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                  disease; cancer
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26-MAY-2000;
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
                                                                                  SI-DVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAID 210
                                                                                                              CSNIHIGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVN 270
                                          stegseitta---sitgsetttastegsetttastegsettsasttgsetttasttsset 112
                                                                                                                                                                                                                167 -----tagse--tipastagsettttstegsetttastegs----etttastess 211
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STLICIVNDALKSSIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDI 151
                                                                                                                                                                                                                                                           271 QYTLAYT-NDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTA---- 324
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analyzing gene expression in human fetal liver -
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30-UNA-2000; 2000US-06084408.
03-AUG-2000; 2000US-053366.
21-SEP-2000; 2000US-023667.
04-CCT-2000; 2000US-023659.
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Gaps

43 TSANPGDTFTLNMPCVFKYTTSQTSVDLTADG------VKYATCQFYSGEEFTTF 91

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Query Match 7.1%; Score 156; DB 22; Length 688; Dest Local Similarity 22.7%; Pred. No. 0.0005; Matches 93; Conservative 64; Mismatches 176; Indels 76;

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expression in human

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample detrived from human heart (see MAAA1535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays is measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed as specification, but was obtained in electronic format directly from WIPO at fite.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe encoded protein SEQ ID NO: 28243.
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                                                                    Single exon nucleic acid probes for analyzing gene hearts -
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7.1%; Score 156; DB 22;
Best Local Similarity 22.7%; Pred. NP. 0.0055;
Matches 93; Conservative 64; Mismatches 176;
                                                                                                                                         Claim 15; SEQ ID No 22519; 530pp; English.
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                     WPI; 2001-488899/53
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fpp.wipo.lnt/pub/published_pct_sequences.
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                                                                                                                                                            7.1%; Score 156; DB 22; Length 688; 22.7%; Pred. No. 0.00055; ive 64; Mismatches 176; Indels 7
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2000us-0207456.
2000us-060408.
2000us-06323687.
2000us-0234687.
2000us-0234587.
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                                                                                                                                                                                        Best Local Similarity 22.78
Matches 93; Conservative
                                                                                             688 AA;
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03-AUG-2000;
21-SEP-2000;
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26-MAY-2000;
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04-OCT-2000;
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16;

176; Indels 76; Gaps

Length 688;

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The present invention provides a number of single exon nucleic acid probles which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
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                                                                                                                                                           Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                           Human bone marrow expressed probe encoded protein SEQ ID NO: 28817.
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analyzing gene expression in human bone marrow -
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22.7%; Pred. No. 0.00055;
ive 64; Mismatches 176;
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-060B40B.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-02346B1.
27-SEP-2000; 2000US-034559.
04-CCT-2000; 2000GB-0024263.
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Best Local Similarity
Matches 93; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
brains -
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
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21-SEP-2000; 2
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Gaps

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The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA15756). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #2847 encoded by probe for measuring placental gene expression
SI-DVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAID 210
                                    113 tmasimgsettmastigsettkvstasskmttvft----ensettiasttasetttvs-- 166
                                                                         211 CSNIHIGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVN 270
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                                                                                                                                                                                            212 etttattigsetttastegsettttstegsetttastegseittvsttgsetttastegs 271
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                                                                                                                                                                                                                                                                                                             368 PIG-ETATVIVDVPYHTTTTVTSEWTGTITTTTTT--NPTDSIDTVVV 413
                                                                                                                                                                                                                                                                                                                                      Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
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Pred. No. 0.00055;
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-060B40B.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-02346B7.
27-SEP-2000; 2000US-0234589.
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                                                                                                                                                                                                                                                                      Peptide #2749 encoded by probe for measuring cervical gene•expression.
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                                                                                                                                                                                                                                                                                                             Probe; human; microarray; gene expression; cervical epithelial cell; cervical cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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7.1%; Score 156; DB 22; Length 689
Best Local Similarity 22.7%; Pred No. 0.0055;
Matches 93; Conservative 64; Mismatches 176; Indels
                  368 PIG-ETATVIVDVPYHTTTTVTSEWTGTITTTTTT--NPTDSIDTVVV 413
                                         328 tagsetttasiegsetttvsstgsetttvsttgtett1tstegsetttv 376
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                                                                                                                                                     AAM16315 standard; Protein; 688 AA
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36-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-050806.
03-MUS-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234587.
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04-OCT-2000; 2000GB-0024263.
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Length 688;

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such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosting, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at fibr.Wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 SI-DVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAID 210
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                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                   Query Match 7.1%; Score 156; DB 22; Length 688; Best Local Similarity 22.7%; Pred: No. 0.00055; Conservative 64; Mismatches 176; Indels 76;
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                                                                                                                                                                                               152 SI-DVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAID 210
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                                       43 TSANPGDIFTLNMPCVFKYTTSQTSVDLTADG-------VKYATCQFYSGEEFTTF 91
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-068408.
03-AUG-2000; 2000US-053366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234587.
04-OCT-2000; 2000GB-0024263.
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23.3%; Pred. No. 0.00096;
.ive 49; Mismatches 181; Indels 128;
                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                               Immobilisation of enzymes to microbial cell wall - by prodn. fusion protein of enzyme linked to anchoring protein
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                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Page 59-64; 99pp; English.
                                                                                                            Toschka H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.1%
Best Local Similarity 23.3%
Matches 109; Conservative
                                                                                                            Klis FM, Schreuder MP,
(UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                                                                                  WPI; 1994-035071/04.
N-PSDB; AAQ54029.
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94 LTCTVNDALKSSIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDI-- 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valuable compounds are isolated from complex mixtures by use of immobilized ligands composed of an anchoring protein and a binding protein. A suitable anchoring protein is yeast FLO1 (associated with flocculation), and a gene encoding a chimeric scFv-FLO1 protein that will anchor in the cell wall of a lower eukaryote, and which binds HCG with high specificity, was produced:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 ygnwgckgmgacsnsggiaywstdlfgfyttptnvtlemtg-----yflppqtgsytf 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immobilised binding proteins for specific cpds - obtd. by expressing chimeric proteins comprising the binding protein and cell wall-anchoring protein in host cells
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                                                                                                                                                                                                                               Binding protein; immobilization; chimeric protein; anchoriting protein; Saccharomyces cerevisiae; flocculation; FLOI gene; scFV; single chain antibody; monoclonal antibody; MAB; human chorionic gonadotropin; HCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verrips CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Geus P, Frenken LGJ, Klis FM, Toschka HY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 36-39; 78pp; English.
AAR58754 standard; Protein; 894 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-EP00427
                                                                                                                 27-MAR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNIL ) UNILEVER NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-279751/34.
N-PSDB; AAQ67360.
                                                                                                                                                                            S. cerevisiae FLO1
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RESULT 1

OB -08 -362-52

Sequence 2. Application US/0836325

APPLICANT: SHERDORS, MARTER P. APPLICANT: SHERDORS APPLICANT: SHERDORS, MARTER P. APPLICANT: SHERDORS, MARTER P. APPLICANT: SHERDORS S. APPLICANT: OR INVERTION: PROTEIN MINHER OF INVERTION: PROTEIN MINHER CONTRICTION: PROTEIN MINHER CONTRICTION: PROTEIN MINHER CONTRICTION: DEATH MADDRESS:

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CLASSIFICATION UNIBER: EP 92202080.5

PRICE APPLICATION UNIBER: EP 92202080.5

PRICE APPLICATION UNIBER: EP 92202080.5

PRICE APPLICATION UNIBER: EP 92203899.7

REFERENCE/CONCET UNIBER: B. 773

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Sequence 2, Appl
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US-08-729-641-4
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PCT-USS5-07-18-19
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US-08-18-74A-43
US-08-78-74A-43
US-08-78-09-18-2
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US-08-78-01-18-19
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Copyright (c) 1993 - 2000 Compugen Ltd
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APPLICATION NUMBER: JP PCT/JP94/00290 FILING DATE: 24-FEB-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 38871/1993 FILING DATE: 26-FEB-1993 ATTORNEY/AGENT INFORMATION: NAME: OBLOW, NORMAN F REGISTRATION NUMBER: 24,618
                                                                                                                                                                         TELEPHONE: 703-412-220
                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
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US-08-325-267A-2
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                                                                                                                                                                                                                                                                        133 SLNFSDGGSSYEYELENAKFFKSCPMLVKLGNQMSDV---VNF-----DPAAFTENVFHS 184
                                                                                                                                                                                                                                                                                                                                                                                              RVMPSLNKVTTLFVAPQCENGYTSG---TMGFSSSNGDVAIDCSNIHIGITKGLNDWNYP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ETGNRTTSEVISHVVTTSTKLSPTATTSLTIAQTSIXSTDSNITVGTDIHTTSEVISDVE 420
                                                                                                                                                                                                                                             61 -YTTSQTSVDLTADGVKYATCQFYSGE-----EFTTFSTLTCTVNDALKSSIKAFGTVTL 114
                                                                                                                                                                                                                                                                                                                        115 PIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAY---LYAS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 QSYNDINADVICEGSNLWITLDEKLYDGEMLWVNALQSLPANVNTIDHALEFQYICLDII 304
                                                                                                                                      Gaps
                                                                                                                                                                                             21 NINDITFSNLEITPLTAN---KQPD-QGWTATFDFSIADASSIREGDEFTLSMPHVYRIK 76
                                                                                                                                                                       10 SFNSLTWSN-----AANYAFKGPGYPTWNAVLGWSL-DGTSANPGDTFTLNMPCVFK-- 60
                                                                                                                                                                                                                                                                                                                                                                                                                       GRSTGYGSFESYHLGMYCPNGYFLGGTEKIDYDSSNNNVDLDCSSVQVYSSNDFNDWWFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 VSSESFSYTKTCTSNGIQIKY-QNVPAGYRPFIDAYIS-ATDVNQYTLAYTNDYTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 SVDKTKTIEILQPIPTTTTTTSYVGVTTSYLTKTAPIGETATVIVDVPYHTTT----
                                                                                                                                    65;
                                                                                                Length 650;
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, WAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TARATA, VOSHIHIRO
APPLICANT: TARATA, VOSHIHIRO
APPLICANT: TARATA, VOSHIHIRO
APPLICANT: TENTILA, MESHIRO
APPLICANT: PENTILLA, MESHIRO
APPLICANT: ONNELA, MAIJA-LEENA
APPLICANT: KREANEN, SIRKKA
TITLE OF INVENTION: YEAST AGGUTINATION GENES AND YEAST
TITLE OF INVENTION: CONTAINING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,267A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                              Query Match 14.1%; Score 308.5; DB 3; Best Local Similarity 25.8%; Pred. No. 1.8e-18; Matches 116; Conservative 79; Mismatches 190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 TISRETASTVVAAPTSTTGWTGAMNTXIPO 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08325267A Patent No. 5585271
    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-362-525-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
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, Carolyn PEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 NWGCKGMGACSNSQGIAYWSTDLFGFYTTPTNV-TLEMTGYFLPPQTGSYTFKFATVDDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 TCTVNDALKSSIKAFGT----VTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 ----KVVYSNAVSWGTLPISVTLP----DGTTVSDDFEG-----YVYSFDD---- 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 ISIDVEFEKSTV-DPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 ----DLSQSNCTVPDPSNYA-VSTTTTTTEPWTGTFTSTSTEMTTVTGTNGVPTDETVIVI 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 NOYTLAYINDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGI----VIVATTRTVTDSTTAVT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 TL-PFNPSVDKTKT----SYVGVTTS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 TTOPWNDTFTSTSTEMTTVTGTNGLPTDETIIVIRTPTTATTAMTTTOPWDDTFTSTSTE 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 YLTKTA----PIGETATVIVDVPYHTT--TVTSEWTGTIT-----TTTTRTN--PTDS 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 NYAFKGPG-YPTWNAVLGWSLD--GTSANPGDIFTLNM------PCVFKYTTSQ-- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 ----YATCQFYSGEEFTTFSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8 1%; Score 177; DB 1; Length 1537; Best Local Similarity 23.0%; Pred. No. 1.5e-06; Matches 112; Conservative 47; Mismatches 181; Indels 146;
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2589-023-0XPCT
TELEPONMUNICATION INFORMATION:
TELEPEN TELEPEN : 703-413-3000
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Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYP
TITLE OF INVENTION: THEIR FUNCTIONA
TITLE OF INVENTION: FOR TREATMENT A
TITLE OF INVENTION: SPECIES INFECTI
                                                                                                                                                                                              TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1537 amino acids
TYPE: amino acids
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, THEIR EUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREAPMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492 LDFTIPPVAGHNSCSIIVGVSGDGKIHVSPYGSKDVSLISAPIOPSELFNEVYCDTCTA- 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 TSANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDAL 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 AGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTTITTSYVGVTTSYL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 KSSIKAFGTVTL----PIAFNVGGTGSSTDLEDS-------KCFTAGTNTVTF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 NDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            586 TTTTGSPSKPTTTTTTTTL--NPILTTT-----TQKPTTTTTKVPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.0%; Score 175; DB 3; Length 1721; Best Local Similarity 23.2%; Pred, NO. 2.76-06; Matches 96; Conservative 41; Mismatches 180; Indels 96;
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Sequence 6, Application US/08928361B
Sequence 6, Application US/08928361B
Setent No. 6071318
SETTLE OF INVENTION: PEPTIDES, POLYPEPTIDES, TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 385 Sherman Avenue, Suite 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-08-700-651-5
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US-08-928-361B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  670 GAIHSGYOTSADFVITT------TTTGAPGQ 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.0%; Score 175.5; DB 3; Length 1837; Best Local Similarity 22.9%; Pred. No. 2.7-06; Matches 93; Conservative 45; Mismatches 176; Indels 93;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: CA
COUNTRY: USA
LIF: 94306-1840
COMPUTER: Tablo Alto
STATE: PAJO6-1840
COMPUTER: Tablo Alto
COMPUTER: Tablo Alto
COMPUTER: Tablo Alto
STATE: PAJO6-1840
COMPUTER: Tablo Alto
COMPUTER: Tablo Alto
SOCTAME: PALOATION NAMER: US,08/928,361B
FILLING DATE: 12-SEP-197
CLASSIFICATION NAMER: US 60/026,062
FILLING DATE: 13-SEP-196
ATTORN WARE: ABO. T6-1(HV)
RECISTATION NUMBER: 480.76-1(HV)
RECISTATION NUMBER: 480.76-1(HV)
TELECOMMUTCATION INFORMATION:
NAME: VEIN, Hana
RECISTATION NUMBER: 480.76-1(HV)
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATICS:
SEQUENCE: ANTON ACTION ACTION
TELECOMMUTCATION INFORMATICS:
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US-08-700-651-5
; Sequence 5, Application US/08700651B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-3618-5
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1100 New York Avenue, N.W. Washington
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                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 TSEGLISTT-----
                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 TSANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDAL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 บารบาบบุญกุษแห่งการการกรุ่นกรุ่นกรุ่นกรุ่นกรุ่นกรุ่นกรุ่นกระจากจะกรุ่นกรุ่นกรุ่นกรุ่นกรุ่น 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 KPTTTTTTTTTTKKPTTTTTTTTTTTTTSETESVIKPDEWCWLEKNGECEAKGATYVGV 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 NDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 GDVAI-----DCS----NIHIGI--TKGLNDWNYPVS-SESFS--YTKTCTSN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 KSSIKAFGIVIL----PIAFNVGGTGSSTDLEDS-------KCFTAGINIVIF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 IGKDGRIENGMAFTMIPNDDTHVRFRFKVKDVGNTISV-----RCRKG--AGKLEFPDRS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          551 ----KYGAIHSGYQTSADFVTTT----------AKPTTTTGAPGQPT 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 AGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTTITTSYVGVTTSYL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 GIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSO(8-362-525-22)
| Sequence 2.2. Application US/08362525 | Sequence 2.2. Application US/08362525 |
| Patent No. 6027910 |
| GENERAL INFORMATION: | APPLICANT: KLIS, FRANCISCUS M. |
| APPLICANT: COSCHEA, MARREN P. |
| APPLICANT: TOSCHEA, HOLSER Y. |
| APPLICANT: COSCHEA, POSCHEA, FOR IMMOBILIZING ENZYMES TO THE TILLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

B.0%; Score 175; DB 3; L

Best Local Similarity 23.2%; Fred. No. 2.7e-06;

Matches 96; Conservative 41; Mismatches 180;
                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/026,062
FILING DATE: 11-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: VEINY, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELEPHONE: 650-324-1677
TELEPHONE: 650-324-1678
                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 1721 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-3618-6
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22;
TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION TITLE OF INVENTION: PROFEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 FSSSNGDVAIDCSNIHLGITKGLND-WNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 LSQSNCTVP-DPSNYAVSTTTTTEPWTGTFTSTSTEMTTVTGTNGVPTD-ETVIVIRTP 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TEPWTGTFTS-TSTEVTTITGTNGQP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 7.1%; Score 155; DB 3; Length 894; Best Local Similarity 23.3%; Pred. No. 5.5e-05; Matches 109; Conservative 49; Mismatches 181; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| |:|||| |: || |: || 50 DSSTYSNAAYMAY---GYASKT-----KLGSVGGQTDISIDYNIPCVSSSGTFPCPQEDS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 LTCTVNDALKSSIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDI-- 151
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                                                                                                                                                                                                                                                                                                                                             COMPUTER READONS 1970
COMPUTER READONS 1970
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATENIN SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENIN RELEASE #1.0, Version #1.25
SOFTWARE: PATENIN DATA:
APPLICATION NUMBER: US/08/362,525
FILING DATE: 04-JAN-1995
FILING DATE: 04-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92202080.5
FILING DATE: 08-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92203899.7
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA: 17-DEC-1992
FILING DATE: 07-JUL-1993
FILING DATE: 07-JUL-1993
FILING DATE: 07-JUL-1993
ATTORNEY/AGRET INFORMATION:
NAME: KOKULIS, DATI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DALL.
ATTORNEY/AGENT INFORMAL.
NAME: KOKULIS, PAUL N.
REGISTRATION NUBBER: 16,773
REFERENCE/COCKET NUBBER: 213289/T7020(V)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELERAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acids
TYPE: amino acids
                                                                                                                                               CUSHMAN DARBY & CUSHMAN, L.L.P.
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319 TDSTTAVTTLPFNPSVDKTKTIEILQPIPTTTITTSYVGVTTSYLTKTAPIGETATVI-V 377

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APPLICANT: DEEGH, JAMES
APPLICANT: BEEGH, JAMES
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCIDES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
FILE REFERENCE: 480.19-4(14)
CURRENT APPLICATION NUMBER: US/08/70,651B
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATECHTIN VEY: 2.0
SEQ ID NO 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: POECESSEN.

TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,

TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGHENTS

TITLE OF INVENTION: SPECIES INFECTIONS

TITLE OF INVENTION: SPECIES INFECTIONS

CORRESPONDENCES: 30

CORRESPONDENCE ADDRESS:

STREET: 385 Sherman Avenue, Suite 6

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 PFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 ITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTTTTTTPDSIDT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
6.9%; Score 150.5; DB 3; Length:
Best Local Similarity 32.5%; Pred. No. 1.2e-05;
Matches 41; Conservative 12; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIE: 94306-1840
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
                   Sequence 12, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/08928361B Patent No. 6071518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 VVVQVP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 TTTKKP 132
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US-08-700-651-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                    TITE OF INVENTION: Immobilized proteins with specific binding tribing trying to the processes and products. The of Invention: capacities and their use in processes and products. WINDER OF SEQUENCES: 40
COMPOTER READABLE PORM:
MEDIUM TYPE: FLOAPY disk
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAREILIR Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/971,692
        :| |:|||| |: || |: 50 DSSTYSNAAYMAY---GYASKT-----KLGSVGGQTDISIDYNIPCVSSSGTFPCPQEDS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 SIDVEFEKSTVDPSAYLYASRVMPSLNKVT--TLFVAPQCENGYT------SGTMG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 FSSSNGDVAIDCSNIHIGITKGLND-WNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 LSOSNCTVP-DPSNYAVSTTTTTEPWTGTFTSTSTEMTTVTGTNGVPTD-ETVIVIRTP 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 FIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 TDSTTAVTTLPFNPSVDKTKTIEILQPIPTTTTTTSYVGVTTSYLTKTAPIGETATVI-V 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 YGNWGCKGMGACSNSQGIAYWSTDLFGFYTTPTNVTLEMTG------YFLPPQTGSYTF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 LTCTVNDALKSSIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDI-- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----FKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFST 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.1%; Score 155; DB 3; Length 894; Best Local Similarity 23.3%; Pred. No. 5:5e-05; Conservative 49; Mismatches 181; Indels 128; Matches 109; Conservative 49; Mismatches 181; Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 NSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCV----
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                                                                                             405 PTSEGLVTTTTEPWTGTFTSTSTEMSTVTGTNGLPTDE-TVIVVKTP 450
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                                                                                                                                                                                                                              Sequence 15, Application US/08971692
Patent No. 6114147
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:

CLASSIFICATION: 435

INCORMATION FOR SED ID NO: 15: SEQUENCE CHARACTERISTICS: .

ELENGTH: 894 amino acids

TYPE: amino acid anto acids

TYPE: amino acid: TYPE: protein

US-08-971-63-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- 69
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Gaps

Indels 11;

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325 VITLPENPSVDKIKTIEILQPIPTITITSYVGVTTSYLTKTAPIGETATVIVDVPYHTT 384
                                                                                                                                                                                                                                                                                                                     265 SATDVNQYTLAYTNDYTCAGSRLOSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTA 324
                                                                                                                                                                                                                                                                                                                                                  Query Match 6.8%; Score 148.5; DB 3; Length 216; Best Local Similarity 31.5%; Pred. No. 2.44-05; Matches 46; Conservative 10; Mismatches 79; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
STREY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WATARI, JUNJI
APPLICANT: TAKATA, YOSHIHRO
APPLICANT: TAKATA, YOSHIHRO
APPLICANT: PENTILA, MESAHRO
APPLICANT: ORNELA, MAJATA-LEENA
APPLICANT: KERANEN, SIRKKA
TITLE OF INVENTION: YEAST AGGLUTINATION GENES AND YEAST
TITLE OF INVENTION: CONTAINING THEM
WUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
219: 2202
COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRATT APPLICATION DATA:
RPLIAG DATE: 18 -NOV-1994
FILING DATE: 18 -NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 38871/1993
FILING DATE: Z6-FEBL-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN P
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2589-023-0XPCT
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP PCT/JP94/00290
FILLING DATE: 24-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 38871/1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 TIVISEWIGIITTTTTTTNPIDSIDT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08325267A Patent No. 5585271 GENERAL INFORMATION:
          INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-3618-8
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US-08-325-267A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 ITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTTTRTNPTDSIDT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69%; Score 150.5; DB 3; Length 175; Best Local Similarity 32:5%; Pred No. 12-605; Matches 41; Conservative 12; Mismatches 72; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306-1840

COMPUTER READABLE FORM:
MEDIUM TYPE: FIO-POPPY disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING_DATE: 12-SEP-1997
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT IMPORMATION:
NAME: Verny, Hana REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
TELECHONE: 650-324-1677
TELECHONE: 650-324-1677
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 175-anino acids
TYPE: anino ACIDS
TOWNICON: 110-acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEPHONE: 650-324-1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-08-928-361B-8
; Sequence 8, Application US/08928361B
; Patent No. 6071518
                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-928-3618-17
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Fri Oct

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Query Match
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APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                 291 PFTLRWTGYKNSDAGSNGIVIVAFTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTT 350
                                                                                                                                                                                                                                                            351 ITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTTTTTNPTDSIDT 410
                                                                                                                                                                                                                                                                                                                             291 PFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTT 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: USA

ZIP: 94306-1804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERANE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: 12-SEP-1997
             Best Local Similarity 33.3%; Pred. No. 4.4e-05;
Matches 40; Conservative 11; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
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6.7%; Score 146.5; DB
Best Local Similarity 33.3%; Pred NO. 4.4e-05,
Matches 40; Conservative 11; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: VEFNY, Hand
REGISTRATION NUMBER: 30.518
REFERENCE/DOCKET NUMBER: 480.76-1(H)
TELECHONICATION INFORMATION:
TELEPHONE: 650-324-1678
ITELEPRAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
ITELENGTH: 249 amino acids
ITELENGTH: 249 amino acids
ITELENGTH: 249 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480.76-1(HV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/08928361B Patent No. 6071518 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein
US-08-928-3618-20
                                                                                                                                                                                                                                                                                                                             g
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US-08-700-651-15
Sequence 15, Application US/08700651B
Sequence 15, Application US/08700.
Septiment of INFORMATION: RECENT, ADMENTION: RECENT, ADMENTION: PROPHYLAXIS AND TREATMENT OF CRYPCOPROTEINS, DNAS AND RNAS TITLE OF INVENTION: POR PROPHYLAXIS AND TREATMENT OF CRYPCOPROTEINS, DNAS AND RNAS TITLE OF INVENTION: POR PROPHYLAXIS AND TREATMENT OF CRYPCOPROTEINS, DNAS AND RNAS FILE REFERENCE: 480.19-4(H)
SCURRENT FILING DATE: 1997-08-14
SEALLER FILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 15.
SEQ ID NO 15.
LENGTH: 249
                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 NKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDW--NYPVSSESFS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 ADGVKYATCQ------FYSGEEFTTFSTLTCTVNDALKSSIKAFGTVTLPIA-- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 EDSYGNWGCKGMGACSNSQGIAYWSTDLFGFYTTPT-------NVTLEMTGY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 FLPPQTGSYT-----SV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 GGATAFNCCAQQQPPITS-----TOFTI---DGIKPWGGSLPPNIEGTV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YTKTCTSNGIQIKYQN-VPAGYRPFI----DAYISATDVNQYTLAYTND------ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 YMYAGYYYPMKVVYSNAVSWGTLPISVTLPDGTTVSDDFEGYVYSFDDDLSQSNCTVPDP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 --YTCAGSRLOSKPFTLRWTGYKNSDA-----GSNGI-----VIVATTRTVTDSTTAV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 FNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAYLYASRVMPSL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 TTLPFNPSVDKTKTIEILQPIPTTTTTSYVGVTTSYLTKTAPIGETATVI-VDVPYHTT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| |:|||| |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |:
                                                                                                                                                                                                                                                                                                                                                                                                       12 NSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFKYTTSQTSVDLT 71
                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 23.3%; Pred. No. 0.00019;
Matches 107; Conservative 45; Mismatches 149; Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 TTTTEPWIGIFISTSTEMSTVTGINGLPIDE-TVIVVKTP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 TTVTSEWTGTITTTTR-----TN--PTDSIDTVVVQVP 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Cryptosporidium parvum
FEATURE:
: LENGTH: 862 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-325-267A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236
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Length 130;

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351 ITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTTTRTNPTDSIDT 410
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                                                                                                                                480.76-1(HV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: October 3, 2002, 16:30:03 Job time: 151 sec
      FILING DATE: 13-SEP-1996

ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30.518
REFERENCE/DOCKET NUMBER: 480.7
FELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
FELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHRRACTERISIS:
LENGTH: 130 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: mino acid
TYPE: mino acid
TYPE: MALEOLEFY: linear
MALECULE TYPE: protein
US-08-928-3618-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 VVVQVP 416
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; Sequence 9, Application US/08700651B
; Patent No. 60158B2
; GENERAL INFORMATION:
; APPLICANT: PETESER. CAROLYN
; APPLICANT: BEECH, JAMES
APPLICANT: URLSON, RICHARD, C.
; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND FILE REFERENCE: 480.10-4(HV)
; TITLE OF INVENTION: NUMBER: 08/41S,751
; CURRENT FILING DATE: 1997-08-14
; CURRENT FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARR PRETICALION UNBER: 08/41S,751
; EARLIER FILING DATE: 1995-04-03
; SOFTWARR PRETICE FILING DATE: 1995-04
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

October 3, 2002, 16:28:17; Search time 20.85 Seconds (Without alignments) 1917.178 Million cell updates/sec Run on:

1 AKTITGVFDSFNSLTWSNAA......TTTTRTNPTDSIDTVVVQVP 416 US-09-715-876-8\_COPY\_17\_432 2190 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 Total number of hits satisfying chosen parameters: 283138 seqs, 96089334 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ			COLUMNIA	
Result No.	Score	Ouery	Ouery Match Length DB	DB		Description
-	2190	100.0	1260	2	860896	aqqlutinin-like pr
7	1907	87.1	1419	7	T30531	
ო	308.5	•	650	~	S22835	alpha-agglutinin -
4	198.5	9.1	948	7	T11678	hypothetical prote
S	177	•	1367	~	S51959	hypothetical prote
9	177		1537	~	S53465	flocculation prote
7	175.5	8.0	1832	~	T31113	mucin-like glycopr
ထ	174.5		973	~	T40778	hypothetical 129.5
0	171.5		456	~	T38221	hypothetical serin
10	171		1251	~	T21389	hypothetical prote
11	167.5	7.6	662	7	A45155	_
12	161.5	7.4	1075	~	S48992	flocculation prote
13	161	7.4	1428	7	AC2224	
14	156.5	7.1	770	~	T22808	
15	156	7.1	851	7	T22696	
16	155	7.1	597	~	B75556	
17	155	7.1	1180	~	E86719	hypothetical prote
18	154.5		1367	-	S48478	_
19	154	7.0	1283	ď	T39174	
20	153.5	7.0	725	~	A41258	a-agglutinin core
21	153.5	7.0		~	T45025	mucin MUC5B, trach
22	153	•		~	S70305	hypothetical prote
23	152		825	~	T29634	
24	152		1902	7	B45764	$\mathbf{\Xi}$
25	151.5		1797	ď	T21889	hypothetical prote
56	151.5	٠.	1805	~	T21888	
27		•	1169	7	S38181	flocculation prote
58	145.5	9.9	648	7	PC4395	mucin 3 - human (f
5	145	9.9	995	~	S50358	hypothetical prote

์ มีสิต	prol	Iacta	hypoth	probabl	hypothe	ہبر	lactocep1)			hypothetical prote	hypothetical prote	hypothetical prote	lactocepin (EC 3.4		hypothetical prote
555862	S25345	A32634	S62518	S56032	S76109	T3424B	206997	T33369	S41819	S67571	T34369	S66852	B44858	B75622	F90696
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1041	1609	1962	609	881	3029	798	1902	1275	522	583	1777	196	1902	691	5291
9.9	9.9	9.9	9.9	9.9	9.9	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.4	6.4	6.4
145	145	145	144.5	144.5	143.5	143	143	142.5	142	142	142	141.5	141	140.5	140
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT

ae sexual

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1260 <HOY> A;Residues: 1-1260 <HOY> A;Cross-references: EMBL:L25902; NID:g704426; PIDN:AAC41649.1; PID:g704427 C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosida

ö ö Length 1260; Indels Ouery Match 100.0%; Score 2190; DB 2; Best Local Similarity 100.0%; Pred. No. 9,2e-136; Matches 416; Conservative 0; Mismatches 0;

1 AKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFK 60

δ

61 YTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKSSIKAFGTVTLPIAFNV 120 17 AKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDFFTLNMPCVPK 76 8 ò g

240 121 GGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKV 180 181 TTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTC ò q à

301 NSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTTTTSYVGVTT 360 8 ò g ò

361 SYLTKTARIGETATVIVDVPYHTTTTVTSENTGTITTTTRTNPTDSIDTVVVQVP 416 q q ŏ

RESULT

4 08:13:54 2002

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Fri

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C; Keywords: glycoprotein
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N.Alternate names: 2X glycoprotein; protein J1418; protein VJR004c
C.Species: Saccharomyces cerevisiae
C.Date: 04-Dec-1992 #sequence_revisiae
C.Date: 04-Dec-1992 #sequence_revisian
C.Accession: $22835; $51229; A32822; $55192; $57019
R;Hauser, K.; Tanner, W.
R;Hauser, K.; Tanner, W.
R;Hauser, K.; Tanner, W.
R;Hauser, K.; Tanner, W.
R;Hauser, M.; Tanner, W.
R;Hauser, M.;Hauser, M.;Hauser, M.;Hauser, M.;Hauser, M.;Hauser, M.;Hauser, M.;Hauser, W.
R;Hauser, M.;Hauser, M.;Hau
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                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: ALA1
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
                 Species: Candida albicans
C; Species: Candida albicans
C; Species: Candida albicans
C; Species: 22-oct-1999 #text_change 17-Mar-2000
C; Species: 22-oct-1999 #sequence_revision 22-oct-1999 #text_change 17-Mar-2000
C; Accession: T30531
R; Gaur, N.K.; Klotz, S.A.
A; Title: Expression, Cloning, and characterization of a Candida albicans gene, ALAl, A; Reference number: Z20847; MUID:98053977
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from CB/EMBL/DDBJ
A; Residues: 1-1419 < CAUJ>
A; CCCSS: Teferences: EMBL:AF025429; NID:92522218; PID:9252219; PIDN:AABB88883.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.1%; Score 1907; DB 2;
86.3%; Pred. No. 3.9e-117;
live 21; Mismatches 36;
agglutinin-like adhesin - yeast (Candida albicans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 86.31
Matches 359; Conservative
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A:Cross_references: EMBL:249504; NID:g1015625; PIDN:CAA89526.1; PID:g1015626; MIPS:YJ
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A) Cross references: EMBL:X87611; NID:g854567; PIDN:CAA60926.1; PID:g854577 R) de Haan, M.; Grivell, L.A.; Smits, P.H.M. submitted to the Protein Sequence Database, September 1995 A; Reference number: S5677 A; Reference number: S5771 A; Accession: S57019 A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-650 <2AG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 LLNSSQTATISLADGTEAFKC-YVSQQAAYLYENTF---TCTAQNDLSSYNTIDGSITF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : :: | | : | | : | 305 ANTTYATQFSTTREFIVYQGRNLGTASAKSSFISTTTTDLTSINTSAYSTGSISTV--- 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 RVMPSLNKVTTLFVAPQCENGYTSG---TMGFSSSNGDVAIDCSNIHIGITKGLNDWNYP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 QSYNDTNADVTCFGSNLWITLDEKLYDGEMLWVNALQSLPANVNTIDHALEFQYTCLDTI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 AGSRLQSKPFTLR----WTGYKNSDAGSNGIVIVATTRTVTD-----STTAVTTLPFNP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 SVDKTKTIEILQPIPTTITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTTT----- 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 -YTTSQTSVDLTADGVKYATCQFYSGE-----EFTTFSTLTCTVNDALKSSIKAFGTVTL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 PIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAY---LYAS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 SLNFSDGGSSYEYELENAKFFKSGPMLVKLGNQMSDV---VNF-----DPAAFTENVFHS 184
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A;Reference number: A32822; MUID:90014768
A;Accession: A32822
A;Molecule type: DNA
A;Residues: 1-448./***
A;Residues: 1-448./***
A;Residues: 1-448./***
A;Residues: 1-478./**
B;Grivellid: PIDN:AAA34417.1; PID:9171044
B;Grivellid: PIDN:AAA344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; cene: SGD:SAG1; AGAL1; AGALPHA1
A; Cross-references: SGD:SO003764; MIPS:YJR004c
A; Map position: 10R
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flocculation protein FtO1 precursor - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein YAR050w
C.Special Scharomyces cerevisiae
C.Special Scharomyces cerevisiae
C.Date: 05-May-1995 #sequence-revision 01-Sep-1995 #text_change 29-Oct-1999
C.Accession: S53465; S43543; S57851; S31205; S57349
R.B.Bussey, H.; Keng, T.; Storms, N.K.; VO, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kasubmitted to the EMBL Data Library, February 1994
A.Reference number: S53458
A.Reference number: S53458
A.Recession: S53465
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A: Residues: 1-1537 < GUS>
A: Cross-references: EMBL: L28920; NID: g1616966; PIDN: AAC09499.1; PID: g694125; MIPS: YAR
A: Rotata, U.; Taretta, Y.; Ogawa, M.; Sahara, H.; Koshino, S.; Onnela, M.L.; Airaksine
Yeast 10, 211-225, 1994
A: Title: Molecular cloning and analysis of the yeast flocculation gene FLO1.
A: Reference number: 843543; MUID: 94262325
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A; Residues: 1-428, M', 430-463, D', 465-473, M', 475-518, M', 520-549, T', 551-608, L', 610
A; Cross-references: BmBL:X78160; NID:9535933; PIDN:CAA55024.1; PID:9535934
A; Cross-references: BmBL:X78160; NID:9535933; PIDN:CAA55024.1; PID:9535934
R; Tean1ssen, A.W.R.H.; Holub, E.; Van der Hucht, J.; Van den Berg, J.A.; Steensma, H
Yeast 9, 423-477, 1993
A; Title: Sequence of the open reading frame of the FLOI gene from Saccharomyces cerev
A; Reference number: S31230; MUID:9289821
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A;Molecule type: DNA
A;Residues: 1-256,927-1516, 'TAYMPVVV' <TEU>
R;Bidard, F: Bony, M.; Blondin, B.; Dequin, S.; Barre, P.
Yeast 11, 809-822, 1995
A;Title: The Saccharomyces cerevisiae FLOI flocculation gene encodes for a cell surfa
A;Reference number: S57349; MUID:96090130
A;Accession: S57349
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                                                                                   163 AILSVGGSIAFECC----AQEOPPITSTNFTIN-----GIKPWNGSPPDNITGTVYMYAG 213
                                                                                                                                               ....-TLPIAFNV-GGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDV 155
                                                                                                                                                                                                     214 FYYPMKIVYSNAVAWGTLPISVTLPDGTTVSDDFEG-----YVYTF---DNNLS--- 259
                                                                                                                                                                                                                                                          156 EFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368 ----PIGETATVIVDVPYHTTT--TVTSEWTGTIT-----TTTTRTN--PTDSIDTVVV 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 TNGLPTDET-IIVIRTPTTATTAMITTQPWNDTFTSTSTEITTVTGTNGLPTD--ETIIV 536
                                 68 VDLTADG-VKYATCQFYSGEEFTTFSTLTCTVNDALKSSIKAF-----GTV---- 112
                                                                                                                                                                                                                                                                                                                260 QPNCTIPDPSNYT-VSTTITTTEPWTGTFTSTSTEMTTVTGTNGVPTDETVIVIRTPTTA 318
                                                                                                                                                                                                                                                                                                                                                                         216 IGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLA 275
                                                                                                                                                                                                                                                                                                                                                                                                                           319 STIITTTEPWNSTFTSTSTELTTVTGTNGVRTDETII-----VIRTPTTATTAITTEP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 YINDYICAGSRLQSKPFILRWIGYKNSDAGSNGI---VIVATTRIVIDSTIAVIIL-PFN 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----IEILQPIPTTTTT-----SYVGVTTSYLTKTA 367
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C;Date: 05-Way-1995 *sequence_revision 01-Sep-1995 *text_change 22-Oct-1999
C;Accession: $51959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  556 TTNAQSSSLSSSNSSALT-----HISSSIVSSGS----SSALSSSTIVSSINSSSSVFI 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP----QCENGY-----TSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFS 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            655 VTETVTSGSV------GPTTTIATPVGST------AGTVLVDIP-TPS 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIP---TTTIT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W-------VTETVTSGSVEFTTIATPVGTTAGTVVVDIPTPSWVTETVT 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 TSYVGVTTSYLTKTAPIGETA-TVIVDVPYHT--TTTVTSEWTGTITTTTTTTNPT-DSI 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSVSSSLQYSSSYVTETTTSGSVGFTTT---IATP----VGSTAGTVVVDIPTPS---W 654
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                                                                                                                                                                                                                                                                                                                                                                                                DSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFKYTTSQTSV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Bussey, H.; Kaback, D.B.; Zhong, W.; Vo, D.T.; Clark, M.W.; Fortin, N. submitted to the EMBL Data Library, August 1994
A: Description: The sequence of chromosome 1 of Saccharomyces cerevisiae.
A: Reference number: S51956
A: Accession: S51959
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8.1%; Score 177; DB 2; Length 1367;
Best Local Similarity 23.3%; Pred. No. 0.001;
Matches 112; Conservative 53; Mismatches 181; Indels 134;
                                                                                                                                                                                                                                                                                  Length 948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ypothetical protein YAL063c - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                           Indels
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-948 «CES»
Cross-references: EMBL.AL031536; NID:e1319499; PID:e1319505
Experimental source: strain 972h(-)
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Residues: 1-136.
Cross-references: EMBL: U12980; GSPDB:GN00001; MIPS:YAL063c
                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                     9.1%; Score 198.5; DB 2; 23.4%; Pred, No. 2.6e-05; tive 74; Mismatches 133;
                                                                                                                                                                                                                                                                                                             al Similarity 23.49
                          A; Molecule type: DNA
A; Kossidues: 1-948 «SEBA
A; Cross references: EMB
A; Experimental source:
C; Genetics:
A; Map position: IIR
A; Nap position: IIR
A; Note: SPBC21D10.06c
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787 GTVLIDVP 794
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Best Local S
Matches 100
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664

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RESULT 8
140778
Inyochhetical 129.5 kd protein - fission yeast (Schizosaccharomyces pombe)
(S.Species: Schizosaccharomyces pombe
(S.Species: Schizosaccharomyces pombe
(C.Species: Schizosaccharomyces pombe
(C.Species: Schizosaccharomyces pombe
(C.Species: Objec-1999 #sequence_revision 03-bec-1999 #text_change 03-bec-1999
(C.Accession: T40778
(S. Marian M.) Barrell, B.G.; Devlin, K.; Churcher, C.M.
(S. Marian M.) Barrell, B.G.; Devlin, K.; Churcher, C.M.
(S. Marcession: T40778
(M.) A.Accession: T40778
(M.) A.Accession
A;Accession: T31113
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule 1ype: DNA
A;Molecule 1ype: DNA
A;Molecules: 1-1832 CBAR>
A;Cross-references: EMBL:AF068065; NID:94063041; PID:94063042; PIDN:AAC98153.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGMAFTMIPNDDTHVRFRFKVKDVGNTISV----RCGKG--AGKLEFPDRSLDFTIPP 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PITITIGSPSKPITITIT------KATITITILNPILITIT-TQKPITITITKVPGKPP1 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 TSANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDAL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAI -- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTTITTSYVGVTTSYLTKTAPI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 TWSTNL-----PTNPTTTAI--YSTSGSS------NITTPYSNRITNSNRITKK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 -- GVKYATCQFYSGEEF-----TTFSTLTCTV------NDALKSSIKAF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 YLSVGTITLTTISGSDLYTSTFPANGTTSGTVEVVIPTAGTVTETAVSGSELYTSTFPAN 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 KSSIKAFGTVTLPIAFNVGGTGSSTDL------EDSKCFTAGTNTVTFNDGDKDI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 TWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFKYTTSQTSV-DLTAD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DCSNIHIGITKGLNDWNYPVSSESFS-----YTKTCTSNGIQIKY
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8.0%; Score 174.5; DB 2; Length 973;
Best Local Similarity 22.6%; Pred. No. 0.001;
Matches 112; Conservative 63; Mismatches 157; Indels 163;
                                                                                                                                                                                                                                                                                                                                          Query Match
8.0%; Score 175.5; DB 2; Length 1832;
Best Local Similarity 22.9%; Pred. No. 0.002;
Matches 93; Conservative 45; Mismatches 176; Indels 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 GETATVIVDVPYHTTTTTTSEWTGTITTTTTTTTDDSIDTVVVQVP 416
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A; Map position: 2
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C;Species: D: Species: Cryptosporidium
R;Barnes, D.A.; Bonnin, A.; Huang, J.X.; Gousset, L.; Mu, J.; Gut, J.; Doyle, P.; Dubrem
Mol. Blochem. Parsaitol. 96, 93-110, 1998
A;Title: A novel multi-domain mucin-like glycoprotein of Cryptosporidium parvum mediates
A;Reference number: 220989; MUID:99066935
                                                                                                                                                                                                                                        A,Map position: IR
CKEWPORTS idplication; glycoprotein; transmembrane protein
CKEWPORTS idplication; glycoprotein; transmembrane protein
CKEWPORTS idplication; glycoprotein; transmembrane protein
CKEWPORTS idplication; propert A2 CRA2-
F; 953-997/Domain: repeat A3 CRA2-
F; 988-1042/Domain: repeat A4 CRA4-
F; 988-1042/Domain: repeat B1 CRA3-
F; 1043-1041/Domain: repeat B1 CRA3-
F; 1251-1347/Domain: repeat B2 (partial) #status atypical CRB2-
F; 1321-1347/Domain: repeat B4 CRB3-
F; 1342-1352/Domain: repeat B4 CRB3-
F; 1406-1467/Domain: repeat C1 CRC1-
F; 1417-1425/Domain: repeat C3 CRC2-
1426-1447/Domain: repeat C3 CRC2-
1426-1447/Domain: repeat C3 CRC3-
1436-1447/Domain: repeat C3 CRC3-
1436-1447/Domain: repeat C3 CRC3-
135,187,262,1114/Weinding site: Carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 ITTTEPWNSTFTSTSTEL-----TTVTGTNGLPTDETIVIRTPTTAMT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 NWGCKGMGACSNSQGIAYWSTDLFGFYTTPTNV-TLEMTGYFLPPQTGSYTFKFATVDDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 TCTVNDALKSSIKAFGT----VTLP1AFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----KVVYSNAVSWGTLPISVTLP----DGTTVSDDFEG-----YVYSFDD---- 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- DLSQSNCTVPDPSNYA-VSTTTTTEPWTGTFTSTSTEMTTVTGTNGVPTDETVIVI 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTPTTASTIITTTEPWNSTFTSTSTELTTVTGTNGVRTDETII-----VIRTPTTATTA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGI---VIVATTRTVTDSTTAVT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TL-PFNPSVDKTKT-----SYVGVTTS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 TTQPWNDTFTSTSTELTTVTGTNGLPTDETIIVIRTPTTATTAMTTTQPWNDTFTSTSTE 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 YLTKTA----PIGETATVIVDVPYHTT--TVTSEWTGTIT-----TTTTRTN--PTDS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 -----YATCQFYSGEEFTTFSTL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | : | | : | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

8.1%; Score 177; DB 2; Length 1537;
Best Local Similarity 23.0%; Pred. No. 0.0013;
Matches 112; Conservative 47; Mismatches 181; Indels 146;
     A;Molecule type: DNA
A;Residues: 1243-1274;1308-1339;1359-1390 <BID>
                                                                                                                                     General SGD:FLO1
Gross references: SGD:S0000084; MIPS:YAR050w
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532 -ETIIV 536
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25;

Gaps

DB 2; Length 973;

Db 342 FTSSPPEYSNSSVIPTSVPSSVSSFTSSNSSYTTLIASNTSITYTGTGGASAFFT 397  Qy 326 TTLPFNPSVDXTKIELLQPIPTTTITTSVGVTTSYLTKTAPIGETATVIVDVPX 381	<u> </u>	Qy         168 LYASRVMPSLNKVTTLEVAPQCENCYTSCTMGFSSSNGDVAIDCSNIHIGITKGLNDWNW 227           Db         770SSKPTPTSTSMTTYNMPTGGTTRTLPSGEI
Db 254 GTTSGTVEVVIPTAGTRTVTKISGSREFTTTTDASGTVSGTVEVVLPTAGTNTMTVVSGS 313  Oy 149 KDISIDVEFEKSTVDPSAYLXASRWPSLN 178  1314 RFFTSVVSASGTVSGCDQTVSGTWGTSETRTTTDASGTRGTVEVVLPTG 373  Oy 179 KVTTLEVAPOCENCYTSGTWGTSSNGDVALDGSNIHIGITKGLNDWTVPVS 231  1	weast (Schilange axt_change jandream, M SPDB:GN0006; glucan	UNITY TABLES.  Best Local Similarity 24.8%; Pred. No. 0.0006;  Matches 110; Conservative 57; Mismatches 147; Indels 129; Gaps 24;  Qy 10 SFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFKYTTSQ65

4 08:13:54 2002

Fri Oct

22;

Gaps

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hypothetical protein all3346 [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp.
Strain PCC 7120)
Species: Anabaena sp.
Strain PCC 7120)
S;Species: Anabaena sp.
C;Species: Anabaena sp.
C;Species: Anabaena sp.
C;Strain PCC 7120)
S;Strain PCC 7120
C;Date: 14-Dec-2001
S;Strain PCC 7120
C;Accession: AC224
R;Stanco, T:; Naramurar, Y:;Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.: Irigu Nakazaki, N.; Shimpo, S.; Squimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
N;Ttile: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: Anabac; MUD:21595285; PMID:11759840
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1428
A;Cross-references: GB:BA000019; PIDN:BAB75045.1; PID:g17132441; GSPDB:GN00179
C;Genetics:
C;Genetics: A;Gene: all3346
                                                                                                                                                                                                                                                                                                                             100 DALKSSIKAFGTVTLPIAFNVGGTGSST-------DLEDSKC-----FTAGTNTV 142
                                                                                                                                                                                                                                                                                                                                                                               219 KVVYSNAVSWGTLPISVELPDGTTVSDNFEGYVXSFDDDLSQSNCTIPDPSIHTTSTITT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                    143 -----TFNDGDKDISIDVEFEKSTVDPSAYLY----ASRVMPSLNKVTTLFVAPQCE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 NGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQ 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 -AGSNGIVIVAT---TRTVTDSTTAVTTLPFNPSVDKTKTIEILQP-----IPTT---- 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVFKYTTSQTSVDLTADGVKYATCQFYSGEBFTTFSTLTCT---vNDALKS------S 105
                                                                                                                                                                                                                                                                           163 AILSVGGSIAFECC----AQEQPPITSTNFTINGIKPWDGSLPDNITGTVYMYAGYYYPL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 TTEPWTGTFTSTSTEMTTITDINGQLTDETVIVIRTPTTASTITTTEPWTGTFTSTE 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 MTTVTGTNGQPTDETVIVIRTPISEGLITTTTEPWTGTFTSTSTEMTTVTGTNG-QPTDE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSD----- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 TVIVIRTPISEGLITTI-----TEPWIGIFISTSTEVI----TITGINGQPIDETVIVIR 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --TITTSYVGVTTSYLTKTAPIGETATVI-VDVPYHTTTTVTSEWTGTIT-----TTTT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 NWGCKGMGACSNSOGIAYWSTDLFGFYTTPINV-TLEMTGYFLPPQTGSYTFSFATVDDS 162
                                                                                                             21 NYAFKGPG-YPTWNAVLGWSLD--GTSANPGDTFTLNM-----PCVFKYTTSQTSVDLT 71
                                                                                                                                                                                                                      72 A----DGVKYATCQFYSGEEFTTFSTLTCTVN----------99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 SLTWSNAAN--YAFKGPGYPTWNAVLGWSLDGTSANPGD-----TFTLNMP 56
         1.4%; Score 161.5; DB 2; Length 1075;
ilarity 2.2%; Pred. No. 0.0083;
Conservative 57; Mismatches 209; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.4%; Score 161; DB 2; Length 1428;
24.5%; Pred. No. 0.013;
tive 43; Mismatches 191; Indels 130;
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Best Local Similarity 24.5°
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 RTN--PTDSIDTVVV 413
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Best Local Similarity
Matches 110; Conserv
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C;Species: Xenopus laevis (African clawed frog)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
C;Accession: A45155
R;Hauser, F:; Hoffmann, W.
Biol. Chem. 267, 24620-24624, 1992
A;Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.: A;Reference number: A45155; MUID:93077556
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A; Residues: 1-1075 <HAC>
A; Cross-references: EMBL:U00029; NID:g551322; PID:g458919; GSPDB:GN00008; MIPS:YHR211w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        locculation protein homolog YHR211w - yeast (Saccharomyces cerevisiae)
Specias: Saccharomyces cerevisiae
Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 29-Oct-1999
Accession: S48992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCRTKGCCFDSSIPQTKWCFYTLSQVADCKVEPSQRVDCGFRG-----ITADQCRQKNCC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 TTTTTKATTTTTP-----TTTTTTKATTTPTT-------TT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 TIPTI-----TTTKATTTTT-----TSGECKMEPSKRE---DCG--YSGITES 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 GTSANPGDIFILNMPCVFKYITSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 LKSSIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKST 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 VDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K----TKTIEILQPIPTTITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTTTTVTSEW 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 GHSHEEHTTTTTKAPTTIQIATTTTTTTTTTTK-------АТРТТТТТТКАТРТ 254
                                                                                                                                                                                                                A;Status: preiminary
A;Status: preiminary
A;Status: preiminary
A;Status: preiminary
A;Colocule (1969: MRNA
A;Cross-references: GB:LO2115; NID:g214147; PIDN:AAA74725.1; PID:g951460
CS:Superfamily: trefoil homology <TRF2>
F;367-347/Commain: trefoil homology <TRF2>
F;367-364/Commain: trefoil homology <TRF2>
F;357-561/Commain: trefoil homology <TRF2>
F;557-61/Commain: trefoil homology <TRF4>
F;573-61/Commain: trefoil homology <TRF4>
F;573-61/Commain: trefoil homology <TRF4>
F;571-61/Commain: trefoil homology <TRF4>
F;571-61/Commain: trefoil homology <TRF4>
F;571-61/Commain: trefoil homology <TRF6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 LNDWNYPVSSESFSYTKTCTSNGIQI -----KYQNVPAGYRPFIDAYISATDVNQYTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 YTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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submitted to the EMBL Data Library, February 1994
A;Description: The sequence of S. cerevisiae cosmid 9177.
A;Reference number: $46671
A;Accession: $48992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.6%; Score 167.5; DB 2;
24.3%; Pred. No. 0.0018;
tive 28; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 TGTITT--TTTRINPIDSIDIVVVQVP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 24.38
Matches 94; Conservative
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A;Gene: MIPS:YHR211w
A;Map position: 8R
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398 TTTRINPIDSIDTVVVQVP 416
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Best Local S
Matches 87
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A:Experimental source: clone F56H9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F56H9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22808
R:Burton, J.
                                                                                                STAIL-----TINPTA-----DTTVESNETVALTLA--SGTGYTVGTT--TAVTGTIT 1031
                                                                                                                                                      DAGSNGIVIVATTRIVID -- STTAVITLPFNPSVDKTKTIEILQPIPTTIT-TSYVGVT 359
                                                                                                                                                                                                                                                                                                      360 TSYLTKTAPIGETATVIVD -- VPYHTTTTVTSEWTGTITTTTTTTTTTTDSID----TVVV 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKAFGTV-----TLPIAFNVGGTGS-STDLEDS--KCFTAGTNTVTFNDGD 148
                                           149 KDISIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVA 208
                                                                                                                                    209 IDCSNIHIGITKGLNDWNYPV----SSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYI 264
                                                                                                                                                                                            -----FTLRWTGYKNS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 TFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKSSIKAF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------GSSTDL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 TTTTLPTTTTMMIPICSLDSLTFGKGDNFQPQVDIDVTYSNLVANIIPGTMDMQSLSTM 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----VDPSAYLYASRVMPSLN------KVTTLFV- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 ILCTSKTLSNFILLTVYFLYIGPTELLYTQIGSMNLNTYLNOTMGLGMYLQGPITQMIT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 --------APQCENGYTSGTM-------GFSSSNG-DVAIDCSNI 214
868 ASTAILTINPTADTTVESNETVALTLASGTGYTVGTTTAVTGTITNDDFPSITLAVSPAS 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Watch 7.1%; Score 156.5; DB 2; Length 770; Best Local Similarity 20.3%; Pred. NO. 0.011; Matches 106; Conservative 48; Mismatches 170; Indels 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: CESP:F56H9.1

Map position: 5

:Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: DNA Residues: 1-770 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Burton, J. submitted to the EMBL Data Library, June 1996 A; Reference number: 219618 A; Accession: T22808
                                                                                                                                                                                            SATDVNQYTLAYTNDYTCAGSRLQSKP-----
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1237 RV 1238
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Cpate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22696
R;Ainscough, R.
A;Reference number: 219601
A;Reference: EMBL: 219601
A;References: EMBL: 219601
A;References: EMBL: 219601
A;References: EMBL: 219601
A;Experimental source: clone F55B11
                                                                                                                                                                                                                                                                                                                                                       374 -----TTTTVP-----TTTTTVPTTTTTVPTTTTTV------VPTTTTV 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 NDWNYPVSSESFSYTKT---CTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTND 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 YTCAGSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486 ТТТVРТТТSVРТТТТVРТТТТVРТТТТVSТТТТVРТТТTVРТТТTVРТТТTVSTTTTVSTTTTV 545
                                                                       461 RV-------PIGFEHIGYYSTPCNNOITIIVVSGIFLIGFLTNFMNFMIGGKLIYT 509
                                                                                                                                                   260 ----IDAYIS-----ATDVNQYTLAYTNDY--TCAGSRLQSKPFTLRWTGYKNSD 303
                                                                                                                                                                                                                 510 WKTLTIFRELSNFKCVMKWISTLLHILLTYKLDVINSCIATSPTADPTT-----TTT 562
                                                                                                                                                                                                                                                                                                      304 AGSNGIVIVATTRIVIDSTIAVTILPFNPSVDKTKTIEILQPIPTTITTSYVGVTTSYL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 KSSIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 DPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 IEILQPIPTTTTTTTSYVGVTTSYLTKTAPIGETA--TVIVDVPYHTTTVTSEWTGTITT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 TSANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDAL 102
215 HIGITKGLNDWNYPVSSESFSYTKTCTSNGIQI------KYQNVPAGYRPF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P------TTTTTVPTTTTVPTTTTVPTTTTVPTTTTVPTTTTTVPTTTTTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 7.1%; Score 156; DB 2; Length 851
I Similarity 23.0%; Pred. No. 0.014;
87; Conservative 32; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  623 TTTTPTTTTST-----TTTTTTTTATPTTTTMPP 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 TKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTTTTNP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: CESP:F55B11.3
A;Map position: 4
A;Introns: 49/3; 123/3; 226/1; 282/3; 669/3; 743/3
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE 1651 / B792;
MEDLINE-9527239; PubMed=7752895;
MEDLINE-9527239; PubMed=7752895;
MEDLINE-9527239; PubMed=7752895;
Candida albicans ALSI: domains related to a Saccharomyces cerevisiae sexual agglutinin separated by a repeating motif.";
MOI. MICTODIOI. 15:39-54 (1995).
I- FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.
I- FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.
I- SIMILARITY: TO YEAST SAGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWASS institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                         streptococc
saccharomyc
saccharomyc
saccharomyc
                                             homo sapien
schizosacch
epstein-bar
dictyostell
saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans (Yeast).

Washaryota, Fungl, Ascomycota, Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
P17955
P03200
Q02817
Q010168
Q101284
P14328
P41809
P11000
P04065
Q04065
Q04179
P29760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat: Signal.
POTENTIAL.
AGGLUTININ-LIKE PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Agglutinin-like protein 1 precursor.
ALSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1260 AA
                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
  NU62_RAT
VGP3_EBV
MUC2_SCHPO
VGP3_EBVA8
SP96_DICDI
HKR1_YEAST
MAPA_STRMU
                                                                                                                                                                                                      YM96_YEAST
DAN4_YEAST
AMYI_SACDI
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Cell adhesion; Glycoprot
SIGNAL
1 17
17
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18 1260
DOMAIN 433 792
REPEAT 433 468
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P46590;
  130
128
127
127
127
126
126
126
128
128
125
125
125
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ALS1_CANAL
  Search time 13.4 Seconds (without alignments) 1202.040 Million cell updates/sec
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074652 candida alb
074652 candida alb
074662 candida alb
074660 candida alb
074660 candida alb
P20840 saccharomyc
P39712 saccharomyc
09550 caenorhabdi
060549 saccharomyc
P6059843 aspergillus
P6059843 aspergillus
P6059843 saccharomyc
P72323 saccharomyc
P72323 saccharomyc
P72521 lactococcus
P72555 saccharomyc
P75555 saccharomyc
P75555 saccharomyc
P75555 saccharomyc
P75555 saccharomyc
P758739 saccharomyc
P758739 saccharomyc
P758739 saccharomyc
P77198 homo sapien
002470 lactobacill
P25655 saccharomyc
P77198 homo sapien
002470 lactobacill
P25652 saccharomyc
P75052 paccharomyc
P75052 saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                        US-09-715-876-8_COPY_17_432
2190
1 AKTITGVFDSFNSLTWSNAA......TTTTRTNPTDSIDTVVVQVP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                     105224 segs, 38719550 residues
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ALS2_CANAL
ALS2_CANAL
ALS2_CANAL
ALS2_CANAL
ALS4_CANAL
SAG1_VEAST
FLO1_VEAST
YQU3_CAEEL
WWH_YEAST
FLO2_VEAST
YQU3_CAEEL
WWH_YEAST
FLO3_CAEEL
WWH_YEAST
FLO3_CAEEL
WWH_YEAST
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VG50_HSV11
CSG_HALVO
CHIT_YEAST
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Maximum Match 100%
Listing first 45 summaries
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SED1_YEAST
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                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                           Title:
Perfect score:
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1907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKSSIKAFGTVTLPIAFNV 120
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                                                                                                                                                                                                                                                                                       LI, Repeal; Signal.
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POLY-THR.
POLY-THR.
POLY-SER.
POLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYK
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  gene, ALA1, that confers adherence properties upon Saccharomyces cerevisiae for extracellular martrx proteins.";
Infect. Immun. 6:5289-5294(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1419;
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87.1%; Score 1907; DB 1;
Best Local Similarity 86.3%; Pred. No. 1.3e-121;
Matches 359; Conservative 21; Mismatches 36;
                                                                                                                                                                                                                                                            EMBL; AF025429; AAB88883.1; -- (CELl adhesion; Glycoprotein; P SIGNAL 1 17 P CHAIN 18 1419 A
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POLY-THR.
N-LINKED (GLCNAC...) (POTENTIAL).
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
Agglutinin-like protein ALA1 precursor (Agglutinin-like adhesin).
ALA1 OR ALS5.
Candida albicans (Yeast).
Eukaryota: Fungi, Ascomycota; Saccharomycotalas; Saccharomycetales; Mitosporic Saccharomycetales; Candida.
NCBL_TAXID-5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYLTKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTTTTTTDSIDTVVVQVP 416
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 4.8e-140;
0; Mismatches 2;
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Best Local Similarity 99.5
Matches 414; Conservative
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                                                                                                                                                                                                                                                                    Hoyer L.L., Payne T.L., Bell M., Myers A.M., Scherer S.; Candida albicans ALS3 and insights into the nature of the ALS gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                            Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TaxID=5476;
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10. Tenet. 33:451-459(1998).

11. FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.

11. PTW: N-GLYCOSYLATED AND O-GLYCOSYLATED (POTENTIAL).
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POTENTIAL.
AGGLUTININ-LIKE PROTEIN 3.
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POLY -
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                                                   Last sequence update)
Last annotation update)
  PRT; 1119 AA
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THR.
THR.
                                                                                       Agglutinin-like protein 3 precursor
                                                                                                                                                                                                                                                   MEDLINE-98309840; PubMed-9644209;
                             (Rel. 38, Created)
(Rel. 38, Last sequ
(Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
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                                                                                                                         Candida albicans (Yeast).
  STANDARD;
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ALS3_CANAL
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86.3%; Score 1889; DB 1; 84.9%; Pred. No. 1.6e-120; Live 30; Mismatches 33;

Ouery Match 86.3 Best Local Similarity 84.9 Matches 353; Conservative

Length 1119;

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                                                                                                                                 181 TILEVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTC 240
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             1 AKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFK 60
                                                                                                                                                                                                                                                                                                                                                      361 SYLTKTAPIGETATVIVDVPYHTTTTVTSEWIGTITTTTTTTTPDSIDTVVVQVP 416
                                                                                                                                                                                                                                                                                                                                                                        Bikaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TAXID-6476.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1773.5; DB 1; Length 468;
Pred. No. 3.6e-113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Agglutinin-like protein 2 precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; Signal.
POTENTIAL.
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80.3%;
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SEQUENCE FROM N.A.
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Best Local Similarity
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61 YITSQTSVDLTADGVKYATCQFYSGEEFITFSTLTCTVNDALKSSIKAFGTVTLPIAFNV 120
                                                                                                                                                                                                                                                                                         121 GGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 NSDAGSNGIVIVATTRTVTDSTTAVTLLPFNPSVDKTKTIEILQPIPTTTTTSYVGVTT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS. MEDILINE-96064684; PubMed-7592821; Chen M. H., Shen Z.-M., Bebin S., Kahn P.C., Lipke P.N.; Structure of Saccharomyces cerevisiae alpha-agglutinin. Evidence for a "Structure of lact wall protein with multiple immunoglobulin-like domains with attpical disulfides."; J. Biol. Chem. 270:26168-26177(1995);
Gaps
                                                                                                                          1 AKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hauser K., Tanner W.; "Purification of the inducible alpha-agglutinin of S. cerevisiae and molecular cloning of the gene."; FEBS Lett. 255:290-294(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYLTKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTTTTTTTDTDSIDTVVVQVP 416
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 34, Last annotation update)
Alpha-agglutinin precursor (AG-alpha-1).
SAG1 OR AGALI OR YATRO04C OR 31418.
Saccharomyces cerevisiae (Baker's yeast).
Elwaryota: Fungli Ascomycota: Saccharomycotina; Saccharomycetes; Saccharomycetales: Saccharomycetales.
    ö
    78; Indels
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Ge Haan M., Smits P.H.M., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/Gengank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 650 AA.
    42; Mismatches
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MEDLINE-90005993; Pubmed-2676603;
Matches 296; Conservative
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P20840;
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DN 11-NOW

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RR 1,10-KA

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MEDITAL MAY T. M., Hecht J.E.;
Hoyer L.L., Payne T.L., Hecht J.E.;
J. Bacteriol. 180:5334-5333(1998).
J. Bacteriol. 180:5334-5333(1998).
J. Bacteriol. Hay PLAY A ROLE IN ADHESION AND PATHOGENESIS.
J. FUNK. N-GIXCOSYLATED AND O-CLYCOSXLATED (POTEWTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYK 300
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                                                                           1 AKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFK 60
                                                                                                                     SYLTKTAPIGETATVIVDVPYHTTTTVTSEWIGTITTTTTTTTTDSIDTVVVQVP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 SYSTKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTTRTNPTDSIDIVVVQVP 431
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Pred. No. 2e-101;
54; Indels
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N. 1 110
N. 18 >469 AGGIUTININ-LIKE PROTEIN 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Agglutinin-like protein 4 precursor (Fragment).
27; Mismatches
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71.28;
Matches 334; Conservative
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Best Local Similarity
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074660;
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SEQUENCE
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FUNCTION: CELL SURFACE GLYCOPROTEIN PROMOTING CELL-CELL CONTACT
TO FACLLITATE MATING. SACCHARDWICES CERENTISIAE A AND ADHA CELL-SELLS
EXPRESS THE COMPLEMENTAR CELL SURFACE GLYCOPROTEINS A-AGGLUTININ
AND ALPHA-, RESPECTIVELY, WHICH INTERACT WITH ONE ANOTHER TO
PROMOTE CELLULAR AGGREGATION DURING MATING.
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                             -i- INDUCTION: BY EXPOSITION TO PHEROMONE (A-FACTOR) SECRETED BY THE PROPOSITE MATING TYPE CELLS (TYPE A).

- PROPOSITE MATING TYPE CELLS (TYPE A).

- PRIN: N-GIXCOSYLATED AND O-GIXCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALPHA-AGGLUTININ.
ACIDIC REGION, PROBABLY IMPORTANT IN
BINDING TO AGGLUTININS OF TYPE A CELLS.
2 X 40 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAC. .) (POTENTIAL).
NAC. .) (POTENTIAL).
NAC. .) (POTENTIAL).
NAC. .).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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N-LINKED (GLCNAC. . . ) (P
N-LINKED (GLCNAC. . . ) (P
N-LINKED (GLCNAC. . . ) (P
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N-LINKED (GLCNAC. ) (F
N-LINKED (GLCNAC. )
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EMBL; X16861; CAA34752.1; --
EMBL; 249504; CAA80926.1; --
EMBL; 249504; CAA89526.1; --
SGD; S0003764; SAG1.
Glycoprotein; Cell adhesion; Si
SIGNAL

20 650 AI
                                                                                                    (POSSIBLE)
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DISULFID
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CARBOHYD
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                    172 RVMPSLNKVTTLFVAPQCENGYTSG---TMGFSSSNGDVAIDCSNIHIGITKGLNDWNYP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 GRSTGYGSFESYHLGMYCPNGYFLGGTEKIDYDSSNNNVDLDCSSVQVYSSNDFNDWWFP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 VSSESFSYTKTCTSNGIQIKY-QNVPAGYRPFIDAYIS-ATDVNQYTLAYTNDYTC---- 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 AGSRLQSKPFTLR----WTGYKNSDAGSNGIVIVATTRTVTD-----STTAVTTLPFNP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 ANTTYATOFSTTREFIVYQGRNLGTASAKSSFISTTTTDLTSINTSAYSTGSISTV--- 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 SVDKTKTIEILQPIPTTITTSYVGVTTSYLTKTAPIGETATVIVDVPYHTT----- 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 PIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAY---LYAS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 ETGNRITSEVISHVVITSTKLSPTATTSLTIAQTSIYSTDSNITVGTDIHTTSEVISDVE 420
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-9286C / AB972;
MEDLINE-95249563; PubMed-7731988;
BUSSEY H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
Storms R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olympia (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Whotherical 138.1 kba protein in FLO9-GDH3 intergenic precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Sakaryota: Fungi: Ascomycota; Saccharomycetina: Saccharomycets
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TAXID-4932.
                                                                                                    Ouery Match 14.1%; Score 308.5; DB 1; Length 650; Best Local Similarity 25.8%; Pred. No. 9e-14; Matches 116; Conservative 79; Mismatches 190; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The nucleotide sequence of chromosome I from Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
-! - SIMILARITY: STRONG, TO YEAST PROFEIN FLOI.
    70339 MW; 8BBF7A1C44C93C2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1322 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 TISRETASTVVAAPTSTTGWTGAMNTYISQ 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
650 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAG3_YEAST
P39712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cerevisiae.
        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
YAG3_YEAST
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REVIEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
   56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 FYYPMKIVYSNAVAWGTLPISVTLPDGTTVSDDFEG-----YVYTF---DNNLS--- 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 NWGCKGIGACSNNPIIAYWSTDLFGFYTTPTNV-TLEMTGYFLPPQTGSYTFKFATVDDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 VDLTADG-VKYATCQFYSGEEFTTFSTLTCTVNDALKSSIKAF-----GTV---- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 -------TLPIAFNV-GGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 EFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 IGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 STIITTTEPWNSTFTSTSTELTTVTGTNGVRIDETII-----VIRTPTTATTATTTEP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 AILSVGGSIAFECC----AQEQPPITSTNFTIN-----GIKPWNGSPPDNITGTVYMYAG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 QPNCTIPDPSNYT-VSTTITTTEPWTGTFTSTSTEMTTVTGTNGVPTDETVIVIRTPTTA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 YTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGI---VIVATTRTVTDSTTAVTTL-PFN 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 WNSTFTSTSTEL-----TTVTGTNGLPTDETIIVIRTPTTATTAMTTTQPWN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 PSVDKTKT-----SYVGVTKTRA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420 DIFISISTELTIVICINGLPIDETLIVIRIPITATIAMTTTOPWNDTFTSTSTELTTVTG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 ----PIGETATVIVDVPYHTTT--TVTSEWTGTIT-----TTTTRTN--PTDSIDTVVV 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                8.1%; Score 177; DB 1; Length 1322;
23.3%; Pred. No. 0.00017;
Live 53; Mismatches 181; Indels 134; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 NYAFKGPGYPTWNAVLG-WSLD--GTSANPGDTFTLNM------PCVFKYTTSQTS 67
                                                                                                                                                                                         (POTENTIAL)
                                                                   Transmembrane; Signal.
                                                                                  POTENTIAL.
HYPOTHETICAL PROTEIN YAL063C.
                                                                                                                                                                                                                                                                                                                                                                                                   AADFDIFF13267CEA CRC64;
                                                                                                                                                                                                                                                                                  (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
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N-LINKED (GLCNAC.

N
                                                                   Glycoprotein;
EMBL, U12980; AAC04971.1; -. SCD; SOU00559; VAL063C.
InterPro; IPR001389; Flocculin.
Pfan; PF00624; Flocculin; 13.
Hypothetical protein; Glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                     138072
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                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                             Best Local Simi
Matches 112;
                                                                                                                TRANSMEM
TRANSMEM
CARBOHYD
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SECONDARYORS CERVISIAE (BAKE'S yeast).

SECONDARYORS CERVISIAE (BAKE'S yeast).

SECONDARYORS CERVISIAE (BAKE'S Yeast).

RE 111_RAIL-15.

RE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 AD--GVKYATCQFYSGEEFT----TFSTLTCTVN--------DALKSSIKAF- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  664 TOTEGCKKTSTISSSSSKFSITPTPTPSSGTTTYNWPTGGTTRTLPSGEIILSESLIAFQ 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 --GTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       724 NCTIVLMQLIYN-----PSTN------KTRTETITDAEGCKKTSSTSKISTIPISPI-- 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           609 PGTTTYN-----WPTGGTTRMLPSGEIILSESLIAYPNCT-TVLMQLIYTPSTNKTRTETT 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----IEILQPIPTTTTTSYVGVTTSYLTKTAPIGE-----TATVIVDVPY 381
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditudae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 PGYPTWNAVLGWSLDGTS------ANPGDTFTLNMPCVFKYTTSQTSVDLT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STASPPTTTYNWPTGGTTRTLPSGEIILSESLIAYKNCTTVLMQLIYNPSTNKTRTETTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 RLQSKP-FTLRW-TGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 770 --SSKPTPTSTSMTTTYNWP---TGGTTRTL----PSGEI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVN--QYTLAYTNDYTCAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            801 -ILSESLIAYKNCTTVLMQLIYN--PSTNKTRTE---TTTDAQGCKATSSTSLKPTSPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.8%; Score 171; DB 1; Length 1251; 23.8%; Pred. No. 0.00041; ative 60; Mismatches 154; Indels 128;
                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sanctation update)
Hypothetical 133.5 kba protein F26C11.3 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMAIN 120 414 SER/THR-RICH.
EQUENCE 1251 AA; 133498 MW; 28959ECA03B9954A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matthews P.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                  PRT; 1251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H-----TTTTVTSEWTGTITTTTTTTVT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, 247072; CAA87369.1; -.
WormPep: PZ6C11.3; CE01561.
InterPro; IPR000436; Sushi_SCR_CCP.
PFam: PF00084; sushi; 1.
SMARY: SM00032; CCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.8% Best Local Similarity 23.8% Matches 107; Conservative
                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                        FZecil.s.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
532 -ETIIV 536
                                                                                                                                        YQU3_CAEEL
Q09550:
                                                                         RESULT 9
YOUN CASE L
10 019-050
DT 011-NOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 --- DLSQSNCTVPDPSNYA-VSTTTTTTEPWTGTFTSTSTEMTTVTGTNGVPTDETVIVI 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGI---VIVATTRTVTDSTTAVT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTOPWNDTFTSTSTEMTTVTGTNGLPTDETIIVIRTPTTATTAMTTTQPWDDTFTSTSTE 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04 NWGCKGMGACSNSQGIAYWSTDLFGFYTTPTNV-TLEMTGYFLPPQTGSYTFKFATVDDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 TCTVNDALKSSIKAFGT----VTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 ISIDVEFEKSTV-DPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 DCSNIHIGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 RIPTTASTIITTEPWNSTETSTELTVTGINGVRIDETII-----VIRTPTTATTA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TL-PFNPSVDKTKT-----SYVGVTTS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 YLTKTA----PIGETATVIVDVPYHTTT--TVTSEWTGTIT-----TTTTRTN--PTDS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 NYAFKGPG-YPTWNAVLGWSLD--GTSANPGDTFTLNM-------PCVFKYTTSQ-- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                       X 20 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 ------YATCQFYSGEEFTTFSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 AILSVGGATAFNCCAQQQPPITSTNFTIDGIKPWGGSLPPNIEGTVYMYAGYYYPM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 ----KVVYSNAVSWGTLPISVTLP-----DGTTVSDDFEG------YVYSFDD----
                                                                                                                                                                                                                                                                                                                                                                                                                                      3 X 9 AA APPROXIMATE TANDEM REPEATS 4-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.1%; Score 177; DB 1; Length 1537;
23.0%; Pred. No. 0.00021;
tive 47; Mismatches 181; Indels 146;
                                                                                                                                                                                                                                                                                                                       51 AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                1226 1392
1226 1342
1342 1342
1340 1342
1408 1416
1417 1425
1425 1434
135 135
135 135
137 434
419 419
419 509
554 654
644 644
689 689
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689 689
681 1114
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                                                                                                               Best Local Similarity
Matches 112; Conserv
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CARBOHYD
SEQUENCE
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CARBOHYD
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287 TTPTT-----TTTKATTTTT-----TSGECKMEPSKRE---DCG--YSGITES 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 QCRTKGCCFDSSIPQTKWCFYTLSQVADCKVFPSQRVDCGFRG----ITADQCRQKNCC 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 7 6%; Score 167.5; DB 1; Length 662; 15 milarity 24.3%; Pred. No. 0.00033; 15 milarity 29; Conservative 28; Mismetches 166; Indels 99; 17 milarity 28; Mismetches 166; 17 milarity 29; 17 milarity 29; 18 m
P-TYPE 3.
12 X APPROXIMATE TANDEM REPEATS,
THR-RICH.
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F085277F1ED2FD40 CRC64;
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TRATITITPITITITITITITIT 505
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67774 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-TYPE 1.
8 x APPROXIMATE TANDEM REPEATS, THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
101-OCT-1994 (Rel. 30, Last annotation update)
101cegumentary mucin C.1 (Fun-C.1) (Fragment).
101cegumentary (African clawed frog).
101cegumentary Metazoa; Chordata; Canniata; Vertebrata; Euteleostomi; Amphlbia, Batrachia, Anura; Mesobatrachia, Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 X 8 AA APPROXIMATE TANDEM REPEATS, ALA/THR-RICH.
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2-8.
P-TYPE 2
                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93077556; PubMed-1447205;
                                                                                                                                                                         01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last seq
01-0CT-1994 (Rel. 30, Last seq
101-0CT-1994 (Rel. 30, Last and
Integumentary mucin C.1 (FIM-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, L02115; AAA74725.1; -. PIR; A45155; A45155.
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-Skin;
                                                                                                                               MUC1_XENLA
Q05049;
                                                                                       RESULT 10
MUC1_XENLA
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                                                                                                                                                                                                                          STRAIN-2288C, AB972,
STRAIN-2288C, AB972,
MEDLINE-94378003; Pubmed-8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Gelsel C., Kirsten J.,
Kucaba T., Hiller L., Jier M., Johnston L., Langston Y.,
Latrellie P., Louis E.J., Macri E., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Files L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Teunissen A.W., Steensma H.Y.;
"Review: the dominant flocculation genes of Saccharomyces cerevisiae constitute a new subtelomeric gene family.";
Yeast 11:1001-1011(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- FUNCTION: MAY BE DIRECTLY INVOLVED IN THE FLOCCULATION PROCESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLOCCULATION PROTEIN FLOS.
REMOVED IN MATURE FORM (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Ekkaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycesowca; Saccharomycesowca; Saccharomycesowca; Saccharomycesowca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Joseph Martin, 1970-1975.

InterPro; IPR01389; Flocculin, Pfam, PF00624; Flocculin, 8.

Glycoprotein; Membrane; Repeat; Cell wall; Signal; GPI-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-ROV-1997 (Rel. 35, Last annotation update)
FLOS OR YHR211W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D151B370B60C8D9F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POCENTIAL).
-- PTW: EXTENSIVELY O-GLYCOSYLATED (PROBABLE).
-- SIMILARITY: BELONGS TO THE FLOCCULIN FAMILY.
                  1075 AA.
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96076625; Pubmed-7502576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, U00029; AAB69731.1; -. PIR; S48992; S48992.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 265:2077-2082(1994).
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                  STANDARD;
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FLOS_YEAST
ID FLOS_YEAST
AC P38894;
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22;

Indels 119;

21 NYAFKGPG-YPTWNAVLGWSLD--GTSANPGDTFTLNM-----PCVFKYTTSQTSVDLT 71

14%; Score 161.5; DB 1; Length 1075; llarity 22.2%; Pred. No. 0.0015; Conservative 57; Mismatches 209; Indels 119;

Similarity

Query Match Best Local Simi Matches 110;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 TEPWIGTETSTSTEMITITIOINGQLIDETVIVIRIPTIASTITITIEPWIGTETSTSTE 338
163 AILSVGGSIAFECC----AQEQPPITSTNFTINGIKPWDGSLPDNITGTVYMYAGYYYPL 218
                                                                                                                                                                                                                                                       100 DALKSSIKAFGTVTLPIAFNVGGTGSST------DLEDSKC-----FTAGTNTV 142
                                                                                                                                                                                                                                                                                                                                  219 KVVYSNAVSWGTLPISVELPDGTTVSDNFEGYVYSFDDDLSQSNCTIPDPSIHTTSTITT 278
                                                                                                                                                                                                                                                                                                                                                                                                             143 -----TFNDGDKDISIDVEFEKSTVDPSAYLY-----ASRVMPSLNKVTTLFVAPQCE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 NGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQ 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 NVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSD----- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 TVIVIRTPISEGLITIT ----TEPWTGTFTSTSTEVT ---- TITGINGQPTDETVIVIR 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 -AGSNGIVIVAT---TRTVTDSTTAVTTLPFNPSVDKTKTIEILQP-----IPTT---- 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 TPTSEGLITTTTEPWTGTFTSTSTEMTTVTGTNGQPTDETVIVIRTPTSEGLISTTTEPW 508
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-!- CATALYTIC ACTIVITY: Hydrolysis of the 1.4-beta-linkages of N-acetyl-Dalucosamine polymers of chitin.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                          72 A-----DGVKYATCQFYSGEEFTTFSTLTCTVN------ 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
NCBL_TaxID-5476;
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MEDLINE-95233977; PubMed-7708682;
MCCreath K.J., Specht C.A., Robbins P.W.;
"Molecular cloning and characterization of chitinase genes from Candida albicans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FPB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
continnase 3 precursor (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567 AA.
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569 GTNGQPTD--ETVIV 581
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P40954;
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CH13_CANAL
1D CH13_CANAL
1D CH13_CANAL
DT 01-F095
DT 01-NOV
DD 01-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 YISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDST 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 -ISKSS-----STTSALSSST 469
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15-DEC-1998 (Rel. 37, Last annotation update)
Exoglucansse I precursor (EC 3.2.1.91) (Exocallobiohydrolase I) (1.4-beta-callobiohydrolase I) (Beta-glucancellobiohydrolase I)
                                                                                                                                                                                                                                                                                                                                                                                TFSTLT-----CTVNDALKSSIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAVITLPFNPSVDKTKTIEILQPIPTTTTTTSYVGVTTSYLTKTAPIGETATVIVDVPYH 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 7.3%; Score 160; DB 1; Length 567;
Local Similarity 20.3%; Pred. No. 0.00087;
es 94; Conservative 46; Mismatches 138; Indels 184; Gaps
                                                                                                                                                                                                                                                                                        225 SFNWDTWLNYAETDSPNKNIKLFVGVPASSRAAGSGYNDPSAVSQYLTSDILNSKYFGGI 284
                                                                                                                                                                                                                                                            10 SFNSLTW------GY 29
                                                                                                                                                                                                                                                                                                                     30 PTWNAVLGWSLDGTSANPGDTFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus aculeatus.
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                          144 FNDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSS
STRAIN-NO. F-50;
Takada G., Kawaguchi T., Sumitani J., Arai M.;
Takada G., Kawaguchi T., Sumitani J., Arai M.;
"Cloning, nucleotide sequence, and transcriptional analysis of
"Spergillus aculeatus No.F-50 cellobiohydrolase I (cbhi) gene.";
J. Ferment. Bloeng. 85:1-9(1988).
-I- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 TTTTVTSEWT-----GTITTT----TTRTNPTDSIDTVVVQ 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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15-DEC-1998 (Rel. 37, Last sequ
15-DEC-1998 (Rel. 37, Last anno
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SEQUENCE FROM N.A.
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059843;
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Best Local S:
Matches 94,
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(1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
(2) EXCOELLOBIOSTES THAT CUT THE DISSACCHARIDE ELLOBIOSE
FROM THE NONREDGLING END OF THE CELLULOSE POLYMER CHAIN;
(3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER SHORT CELLO-OLIGOSACCHARIDES TO GLUGOSE.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-beta-D-glucosidic linkages in cellulose and cellotetraose, releasing cellobiose from the non-reducing ends of the chains.
-!- SIMILARITY: BELONGS TO CELLULASE FAMILY 7 OF GLYCOSYL HYDROLASES).
-!- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 VGGYINCYSGNIWDSSICSIDITCASECALEGATYESITGV-----TISGSSLRLN 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPGKTVDNSKPFTVVTQFITHDGTDTGTLTEIRRLYVQNGVVIGNGPSTYTAASGNSITE 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 KAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 DADGGVS-RFPINKAGAKYGTGYCDSOC---PRDLKFIDGQANIE---GWEPSSTDVNA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 YL-YASRVMPSL----NKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 TCAGSRLQSKPFTL--RWTGYKNSDAGS------NGIVI-----VATTRTVT- 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 7.1%; Score 156; DB 1; Length 540; Best Local Similarity 21.4%; Pred. No. 0.0015; Matches 112; Conservative 7; Mismatches 163; Indels 192; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB002821; BAA25183.1; -.
HSSP, P00725; JAZ6.
InterPro; IPR000254; CBD_fungal.
InterPro; PR0001722; Glyco_hydro_7.
Pfam: PF00744; CBD_1; Jyco_hydro_7.
Pfam: PF00744; CBD_1; Jyco_hydro_7; 1.
Pfam: PF00744; GLHVDRADSE.
Pr0Dom; P0001821; CBD_fungal; 1.
Pr0Dom; P0186135; GLyco_hydro_7; 1.
SMART; SM00325; fCBD_ FUNGAL; FALSE_NEG.
PROSITE; PS00562; CBD_FUNGAL; FALSE_NEG.
CELLUIOSe degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ITGVFDSFNSLTWSN------AANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLN 54
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N-LINKED (GLCNAC. .) (POTENTIAL)
002D7FD28DF194D0 CRC64;
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NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
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BY SIMILARITY
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PIR; S48478; S48478.
SGD; S0001458; MUC1.
Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein; Signal; Multigene family.
Signal; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
Agglutinin attachment subunit precursor.
AGAI OR YNRO44W OR N3431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 725 AA.
                                                                                                                                  136110
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1367
817
874
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210 1367
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1367 AA;
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P32323;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-31 FROM N.A.
SEQUENCE OF 1-31 FROM N.A.
STRAIN=SEXIO1-1C;
WINDLINE-89031230; PubMed-3141213;
Pardo J.M., Ianez E., Zalacain M., Claros M.G., Jimenez A.;
Pardo J.M., Ianez E., Falacain M., Claros M.G., Jimenez A.;
Familar short elements in the 5' regions of the STA2 and SGA genes from Saccharomyces cerevisiae.";
FEBS Lett. 239:179-184(1988).
-:-CATALYTY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chains
with release of beta-D-glucose.
-:-SIMILARITY: SOME SPECIS: 13.
-:-SIMILARITY: SOME, TO S. POMBE SPECISE: 13C.
               -----DSTTAVTTLP 329
                                          359 SFCKAEKTLFGDINVFETHGGLSAMGDALGDGMVLVLSLWDDHAADMLWLDSDYPITSCA 418
                                                                      330 FNPSVDKTKTIEILQPIPTTITTSYV--GVTTSYLT----KTAPIGET----- 372
                                                                                             419 SSPGVAR-----GTCPTTGNATYVEANYPNSYVTYSNIKFGTLNSTYSGTSSGGSSS 471
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-S288C, AB972;
BATCHI B.G. AB972;
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A., Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M., Louis E., Lye G., Woule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walbh S. V., Whitehead S.; Bublicked (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                  AMYH_YEAST STANDARD; PRT; 1367 AA.

MAYH_YEAST
01-806640; P08068;
01-806-19988 (Rel. 13, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 40, Last annotation update)
01-Corr_2010 (Rel. 40, Last annotation update)
01-Corr_2010 (Rel. 40, Last annotation update)
01-FEB-1995 (A.4-alpha-D-glucan glucohydrolase).
STA1 OR STA2 OR MAL5 OR YIR019C,
Saccharomyces Grevislae (Baker's yeast).
SACCHAROMYCEAST Fungi: Ascomycotta; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamashita I., Nakamura M., Fukui S.;
Gene fusion is a possible mechanism underlying the evolution
                                                                                                                                SEQUENCE OF 1-242 AND 762-1331 FROM N.A. MEDLINE-87194600; Pubmed-3106330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol. 169:2142-2149(1987).
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SEQUENCE FROM N.A.
MEDLINE-91304412; PubWed-2072914;
Roy A. Lu C.F., Marykwas D.L., Lipke P.N., Kurjan J.;
The AGAL product is involved in cell surface attachment of the Saccharomyces codrustate cell adhesion glycoprotein a-agglutinin.";
Mol. Cell. Biol. 11:4196-4206(1991)
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POPENTIAL.
GLUCOANYLASE $1/$2.
SEXTHR-RICH.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MW; 91C00E2DBD61AA9D CRC64;
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Kakaryote; Fundi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.1%; Score 154.5; DB 1; Length 1367; Best Local Similarity 23.6%; Pred No. 0.006; Matches 115; Conservative 40; Mismatches 184; Indels 149;
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STVDPSAYLYASRVMPSL-NKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGI 218

160

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           3 X APPROXIMATE TANDEM REPEATS, SER/THR-
                                                                                 -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR AND/OR BY CARBOHYDRATE-MEDIATED COVALENT CROSS-LINKS (POSSIBLE).
                                                                                                                                                                                                                                        A-AGGLUTININ ATTACHMENT SUBUNIT.
2 X APPROXIMATE REPEATS.
                                                                                                                                                                                                                 Signal; GPI-anchor; Repeat;
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PIR; A41258.
SGD: S0005327; A631.
Glycoprotein; Cell adhesion;
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725 AA;
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Length 725;

IAFNVGGTGSSTDLEDSKCFTAGTNTVTF-------NDGDKDISIDVEFEK 159 264 SSTSTSSSSTSTSPSSKSTSASSTSTSYSTSTSPSLTSSSPTLASTSPSSTSTFTD 323

116

61 YTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDAL----KSSIKAFGTVTLP 115

163 ASIISPVTSTLSSTTSSN------PTTT-----SLSSTSFSSTST--SPSSTS 204

AKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFK 60

7.0%; Score 153.5; DB 1; 21.9%; Pred. No. 0.0032; tive 64; Mismatches 209;

Query Match Best Local Similarity 21.9% Matches 95; Conservative

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278
        381
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                                                                                279 DYTCA-GSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKT 337
                                                                                                        435 ATVCTHESCMPSOTTSLITSSIKMS -- - TKNVATSVSTSTVESSYACSTCAETSHSYSSV 491
TKGLNDWNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTN
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1 AKTITGVEDSFNSLTWSNAA......TTTTRTNPTDSIDTVVVQVP 416
                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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2: sp_batteria:*
3: sp_fung1:*
4: sp_human:*
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1: sp_vertebrate:*
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Ouery

No. Score Match Length DB ID

Description

RT "The ALS5 gene of Cand	RT terminal domain.":	RL Yeast 18:49-60(2001).	DR EMBL; AF068866; AAD328	SQ SEQUENCE 1270 AA; 1			Ouerv Match 8.	Best Local Similarity 8	Matches 362: Conservati		OV 1 AKTITGVFDSFNSLTWS		Db 17 AKATEGIFNSIDSLEWS		Ov 61 YTTSOTSVDLTADGVKY		Db 77 FTASOKSVDITADGVKV		Ov 121 GGTGSSTDLEDSKCFTA	
			Description		Q9y743 candida alb	093865 candida alb	Q9urq0 candida alb		candida	candida	09v8f2 candida alb	candida	O9hf72 candida dub	candida		candida	candida	candida	candida	•••
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			Lengt		127(	1047	466	1523	469	466	144	336	338	33]	229.	43	35	126	12,	'n
	<b>,</b>	Query	Match		87.8	86.3	90.0	73.3	73.2	73.2	70.7	67.2	54.4	53.7	45.5	45.2	44.8	16.4	15.6	10.0
			Score		1922	1889	1764.5	1605	1604	1602.5	1549	1471	1191	1176	997.5	990.5	981	359.5	341	219

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					Gaps 'K 60       76	120 136 180
			tes;	ż	tch al Similarity 87.8%; Score 1922; DB 3; Length 1270; al Similarity 87.0%; Pred. No. 1.7e-116; 362; Conservative 20; Mismatches 34; Indels 0; Gc ANTICYDSENSILWANANIVERSIDGTSANFODFTLINNFOVFK ANTICIFICIAL IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	YTTSOTSVDLTADGVKYATCOFYSGEETTESTLTCTVNDALKSSIKAFGTVTLPIAFNV :
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		PRT; 1270 AA. Created) Last sequence update) Last annotation update)	charc and 1de	the /	Length 1270; Indels 0 ANPGDTFTLNMP	KAFGI         KAFGI 
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	NRY;	el. 12, el. 12, el. 19, el. 19,	ist). comycc itospo	Med-1	87.8%; 87.0%; Elve 2 «SNAANYA 	YATCC        XATCC
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	T 1 3 09Y743	09Y743; 01-NOV-1999 (TrEMBLrel. 01-NOY-1999 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.	Candida albicans (Yeast). Candida albicans (Yeast). Eukaryota; Fungi; Ascomycota; Saccharomycetales; mitosporic NCBI_TaxID-5476;	SEQUENCE FROM N.A. STRAIN-1161; MSDLINE-21064501; Pubmed-11124701; Hoyer L.L., Hecht J.E.; "The ALSS gene of Candida albicans terminal domain."; Yeast 18:49-60(2001). EMBL; AF066866; AAD22849.1; SEQUENCE 1270 AA; 133337 MW; D	Query Match Best Local Similarity Matches 362; Conserv I AKTITGVENSENSI	61 Y 77 E 121 G
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Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1) SQUENCE FROM N.A. STRAIN-ArCC10261; Mishart J.A., Wu H., Brown A.J.P.; STRAIN-ArCC10261; Mishart J.A., Wu H., Brown A.J.P.; Leng P., Lee P.R., Wishart J.A., Wu H., Brown A.J.P.; Alsofuence of the hypha-specific, agglutinin-like cell surface packed (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF051313; AAD02580.1; -- SEQUENCE 1047 AA; 111944 MW; C2327659AA911F2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.3%; Score 1889; DB 3; Length 1047; 84.9%; Pred. No. 1.9e-114; Live 30; Mismatches 33; Indels 0;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AGGLUTININ-LIKE CELL SURFACE PROTEIN.
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Best Local Similarity 84.99
Matches 353; Conservative
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WEDLINE-98440424; PubbHed-9765564;

HOYEL L. L. Payne T.L., Hecht J.E.;

Tadentification of Candida albicans ALS2 and ALS4 and localization of als procedus to the fungal cell surface.";

J. Bacteriol. 180:5344-543(1998).

EMBL; AF024582; AAC64237.1;

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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
AGGLUTININ-LIKE PROTEIN (FRAGMENT)
Candida albicans (Yeast)
Eukaryota, Saccharomycetiaes; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                        Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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Q9URQ0 PRELIMINARY; PRT; 468 AA.
09URQ1 09URQ1 01-MAY-2000 (TrENBLrel. 13, Last sequence update)
01-MAY-2000 (TrENBLrel. 13, Last sequence update)
01-MAY-2000 (TrENBLrel. 13, Last annotation update)
AGGLUTININ-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                     Match 80.6%; Score 1764.5; DB:
Local Similarity 79.8%; Pred. No. 8.7e-107
GS 332; Conservative 28; Mismatches 55
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Candida albicans (Yeast).
Candida albicans (Yeast).
Cardyca: Fungl; Ascomycota; Saccharomycetales; mitosporic
W.N.I.TaxID=5476;
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TAXID=5476;
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoyer L.L., Hecht J.E., Mirus K.A.;
The ALS9 gene of Canadida albicans.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AF229989; AAK00764.1;
NOW TER 468
SEQUENCE 468 AA; 50127 WW; B291D3EB15FB96DE CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
AGGLUTININ-LIKE PROTEIN (FRAGMENT).
   77;
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   Conservative 43; Mismatches
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Best Local Similarity
Matches 298; Conserv
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   Matches 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9C471
Q9C471;
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                                                                                                                                                                                                                                                                                  181 TILFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTC 240
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                                                                                                                                                                                                                                                                 61 YTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKSSIKAFGTVTLPIAFNV 120
                                                                                                                                                                                                                                                                                                                     121 GGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKV 180
                                                                                                                                                                                                                                                                                                                                                                                                                             241 TSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 NSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTTTTSYVGVTT 360
                                                                                                                                                                                                                             1 AKTITGVFDSFNSLTWSNAANYAFKGPGYPTWNAVLGWSLDGTSANPGDTFTLNMPCVFK 60
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WEDLINE-9840424; PubMed-9765564;
WEDLINE-98404024; PubMed-9765564;
"Identification of Candida albicans ALS2 and ALS4 and localization of als proteins to the fungal cell surface.";
J. Bacteriol. 180:5334-5348; SAG64241.1;
"MON_TER 469 AA; 49597 MW; 88BC96D79142C8DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 SYLTKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTTTTTTTDSIDTVVVQVP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALS4.

Gandida albicans (Yeast).

Eukaryota: Fungi: Ascomycota: Saccharomycetes:
Saccharomycetales: mitosporic Saccharomycetales: Candida.

NCBI_TaxID=5476:
                                                                                                                                                             Length 1523;
                                                                                                                                                                                     76; Indels
                                                 Chen X., Chen J.-Y.;

*Last (agglutinin-like sequence) of Candida albicans.";

*Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

BENEL AF272027; AAG25054.1;

NON TER 1523 AA; 159168 MW; 73AF3B3E442FD53C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
AGGLUTININ-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                          73.3%; Score 1605; DB 3; 70.9%; Pred. No. 7.3e-96; tive 45; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 AA
                                                                                                                                                            Query Match 73.39
Best Local Similarity 70.99
Matches 295; Conservative
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                        SEQUENCE FROM N.A.
NCBI_TaxID=5476;
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TTLFVAPQCENGYTSGTWGFSSSNGDVAIDCSNIHIGITKGLNDMNYPVSSESFSYTKTC 240

181

Length 469;

Score 1604; DB 3; Pred. No. 2.2e-96;

73.28; 71.28;

Ouery Match Best Local Similarity

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Best Local Similarity 81.0%
Matches 272; Conservative
                                   PRELIMINARY;
                                                                                                                                                                          SEQUENCE FROM N.A.
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Q9HF70;
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197 SSLFVVPQCENGYTSGIMGFVASNG-ATIDCSNVNIGISKGLNDWNFPVSSESFSYTKTC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKSSIKAFGTVTLPIAFNV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 AKTISGVFTSFNSLTYTNTGNYPYGGPGYPTWTAVLGWSLDGTLASPGDTFTLVMPCVFK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AGGLUTININ-LIKE PROTEIN 6.
AGGLUTININ-LIKE PROTEIN 6.
Candida albicans (Yeast).
Eukaryote: Yungi, Ascomycota: Saccharomycotina; Saccharomycetales;
NGBL_TaxID-5476;
NGBL_TaxID-5476;
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MEDLINE-20321177; PubMed-10861907;
MEDLINE-20321177; PubMed-10861907;
The ALS6 and ALS7 genes of Candida albicans.";
EMBL, AF075293; AAD42033.1; -
InterPro: IRR03015; HLLLAY.
ENGSTITE; SS00038; HELIX.LOOP.HELIX; UNKNOWN.1.
SEQUENCE 1443 AA: 151476 MW; DCBD693F4C435809 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.7%; Score 1549; DB 3;
68.7%; Pred. No. 2.9e-92;
11ve 54; Mismatches 75;
                                                                                                                                                                                                 PRT; 1443 AA.
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Best Local Similarity 68.7
Matches 287; Conservative
                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                             Q9Y8F2
Q9Y8F2;
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225 WNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAG 284
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                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida. NCBL_TaxID-42374;
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Candida.
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Hoyer L.L., Hecht J.E., En J., Kapteyn J.C., Klis F.M.;

Exidence suggesting the presence of an ALS gene family in dubliniensis and Candida tropicalis.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, ARCOSCA3, ARGASCA3.2;

NON_TER 1

NON_TER 316

SEQUENCE 336 AA: 35593 MW; E513E6EA9EBEBEC7 CRC64;
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Hoyer L.L., Hecht J.E., En J., Kapteyn J.C., Klis F.M.;
                                                                                    01-MAR-2001 (TrEMBLrel. 16, Greated)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 17, Last annotation update)
AGGLUTININ-LIKE PROTEIN ALSD2P (FRAGMENT)
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Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; MCBI_TaxID-42374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.2%; Score 1471; DB 3;
81.0%; Pred. No. 6.2e-88;
iive 31; Mismatches 33;
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                                                                                                                                                                                                                                                                                                            Candida dubliniensis (Yeast).
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300 KNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNBSVDKTKTIELLQPIPTTTTTTSYVGVT 359
318 LYDEALAIGADLVRTSSYLGSTRTTTLPFSRLÖKTKTLVLDEPPPTTYTFSHRGED 377
     121 GGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDPSAYLYASRVMPSLNKV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 TNFVMSTPCFMGYQSGKLGFTSNDDDFEIDCSSIHVGITNEINDMSMPVSSVPFDHTIRC 257
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                                                                                                                                                                                          285 SRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQ 344
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                                                       165 SAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLND 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enkaryota: Fungl; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharowycetales; mitosporic Saccharomycetales; Candida.
NCBL_maxID=5476.
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                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DC-2001 (TrEMBLrel. 19, Last annotation update)
AGGLUTININ-LIKE PROTEIN ALS7P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 45.5%; Score 997.5; DB 3; Best Local Similarity 47.0%; Pred. No. 2.8e-56; Matches 196; Conservative 71; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIANA-2231177; Pubmed-10861907;
HOYER L.L., Hecht J.E.;
HOYER LS. and ALST genes of Candida albicans.";
Yeast 16:847-855(2000).
EMBL. AF201684; AAF98068.1; -
SEQUENCE 2297, AA; 244723 WW; 59B020C63027F65
                                                                                                                                                                                                                                                                                                                                                                               2297 AA
                                                                                                                                                                                                                                                          ALS7.
Candida albicans (Yeast).
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQ--YTLAYTNDYTC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 AGSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEI 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TDGKKGNDPLIYFWTSYTNSDAGSDGAVVIVITKTVTDSTTAITTLPFDPTVDKTKTIEV 300
                                                                                                                                                                                                                        45 ANPGDIFTLNMPCVFKYTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKS 104
                                                                                                                                                                                                                                                                                           SIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVDP 164
                                                                                                                                                                                                                                                                                                                                                           SAYLYASRVMPSLNKVTTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLND 224
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                                                                                                                                                                                                                                          1 ANAGDTFTLNMPCVFKFITDQTSVDLVADGRTYATCDLYSGEEFTTFSSLKCTVSNALNS 60
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"Evidence suggesting the presence of an ALS gene family in Candida dublintensis and Candida tropicalis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
BENBL: AF201685; AAG35603.1; -.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        candida dubliniensis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TaxID-42374;
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                                                                                                                                                        Length 338;
                                                                                                                                                                                        66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 331 331
SEQUENCE 331 AA; 35297 MW; 469AB72F9CE029BF CRC64;
                                                                                   338 338
338 AA; 35908 MW; COA7F2F94609E172 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                    Ouery Match 54.4%; Score 1191; DB 3; Best Local Similarity 64.8%; Pred. No. 8.7e-70; Metches 219; Conservative 51; Mismatches 65;
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01-WAR-2001 (TREMBLrel. 16, Last sequence
01-JUN-2001 (TrEMBLrel. 17, Last annotation)
AGGLUTININ-LIKE PROTEIN ALSD3P (FRAGMENT)
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SEQUENCE
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Q9HF69
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"Characterization of agglutinin-like sequence genes from non-albicans candida and phylogenetic analysis of the ALS family."; canetics 157.1555-1567(2001).

EMBL; AF211866; AAG4533.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 DWNYPVSSESFSYTKTCTSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 GSRLQSKPFTLRWTGYKNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEIL 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 SSIKAFGTVTLPIAFNVGGTGSSTDLEDSKCFTAGTNTVTFNDGDKDISIDVEFEKSTVD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 13803;
Hoyer L.L., Herbt J.E., En J., Kapteyn J.C., Klis F.M.;
Evidence suggesting the presence of an ALS gene family in Candida dubliniensis and Candida tropicalis ";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF201686; AG35604.1; -.
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STRAIN-ATCC 13803;
MEDLINE-211866039; Pubmed-11290712;
HOYOT L.L., Fundyga R., Hecht J.E., Kapteyn J.C., Klis F.M.,
Arnold J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.8%; Score 981; DB 3; Length 353;
llarity 54.9%; Pred. No.,3.7e-56;
Conservative 50; Mismatches 100; Indels
Saccharomycetales; mitosporic Saccharomycetales; Candida. NCBI_TaxID=5482;
                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 353 353
SEQUENCE 353 AA; 37272 MW; 4268154D5615DE08 CRC64;
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126 AA; 13419 MW; D28914A425526888 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AGGLUTININ-LIKE PROTEIN ALST3P (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida tropicalis (Yeast)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 185; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
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Q9HF49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTLFVAPQCENGYTSGTMGFSSSNGDVAIDCSNIHIGITKGLNDWNYPVSSESFSYTKTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 TNFVMSTPCFMGYQSGKLGFTSNDDDFELDCSSIHVGITNEINDWSMPVSSVPFDHTIRC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YTTSQTSVDLTADGVKYATCQFYSGEEFTTFSTLTCTVNDALKSSIKAFGTVTLPLAFNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TSNGIQIKYQNVPAGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWT-GY 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 KNSDAGSNGIVIVATTRTVTDSTTAVTTLPFNPSVDKTKTIEILQPIPTTITTSYVGVT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 TSYLTKTAPIGETATVIVDVPYHTTTTVTSEWTGTITTTTTRTNPTDSIDTVVVQV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALS7.
Candida albicans (Yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09HF71;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last senotation update)
AGGLUTININ-LIKE PROTEIN 1 (FRAGMENT).
ALSTI tropicalis (Yeast).
Candida tropicalis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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45.2%; Score 990.5; DB 3; Length 433;
Best Local Similarity 46.9%; Pred. No. 1.1e-56;
Matches 195; Conservative 71; Mismatches 149; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 433 4837 MW; 1F30CFD99C2EC445 CRC64;
                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AGGLUTNIN-LIKE PROTEIN 7 (FRAMBENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-1161;
STRAIN-1161;
BODELINE-20321177; PubMed-10861907;
HOPEr L.L., Hecht J.E.;
The ALSS and ALS7 genes of Candida albicans.";
Teat 16:847-855(2000).
EMBL; AF075294; AAA42034.1; -.
BOUN_TER 433 AA; 48037 WW; IF30CFD99C2EC445
                                                                                                                                                                                                                        433
                                                                                                                                                                                                                        PRT;
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                                                                                                                                            RESULT 12
0978F1
1D 0978F1
DT 01-NOV
DT 01-DEC
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09HF71
10 09HF71
AC 09HF71
DT 01-MAR
DT 01-MAR
DT 01-MAR
DF AGGLUT
GN ALST1.
OS CANDIG
OC EUKALY
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Genetics 157:1555-1567(2001).
EMBL: AF211865; AAG43532.1; -...
                                                                                                                            254 AGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGIVIVA 313
                                                                                                                                                                                                                                                                                                                                                           60 TIITGIQSNIIVTLPENPRADHIKIIEVIVPIPTVITTISXIGVITSYIITGTIGDIA 119
                                                                                                                                                                                                                                                                                                            314 TTRIVIDSTIAVTIPPENPSVDKTKTIEILQPIPTTTITTSYVGVTTSYLTKTAPIGETA 373
Best Local Similarity 55.1%; Pred. No. 2.1e-16;
Matches 70; Conservative 15; Mismatches 41; Indels 1; Gaps
                                                                                                                                                                                     Candida tropicalis (Yeast).

Valakaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

VGBI_TaxID-5482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEĞUENCE FROM N.A.
STRAIN-ATCC 13803.
MEDLINE-21186039; Pubmed-11290712;
HOyer L.L., Fundyga R., Hecht J.E., Kapteyn J.C., Klis F.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 15.6%; Score 341; DB 3; Length 127; Best Local Similarity 51.2%; Pred. No. 3.4e-15; Matches 65; Conservative 22; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 127 127
SEQUENCE 127 AA; 13668 MW; 178E25AA919EF387 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DC-2001 (TrEMBLrel. 19, Last annotation update)
AGGLUTININ-LIKE PROTEIN ALST2P (FRAGMENT).
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254 AGYRPFIDAYISATDVNQYTLAYTNDYTCAGSRLQSKPFTLRWTGYKNSDAGSNGIVIVA 313

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